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BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

Field of the Invention

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

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Background to the Invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

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These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

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Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

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(57) Title: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a reagent for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

WO 02/064766 A2

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oltvai and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Saito *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996). Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeier *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear. It is an aim of the present invention to provide new bax sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (a) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi. It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian bax gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic BAX gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*.

Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida* spp. homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 600, 602, 604, 606, 608, 610, 612, 614,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1994), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi

selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional

equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412,

414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,

37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - 10 (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
 - 15 (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
 - 20 (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
 - 25 (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
 - 30 (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to f), (g) the complement of any of the nucleic acids as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.
- The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergilliosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof. The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector, wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising to a human homologue of at least one yeast or candida nucleic acid described herein.

10 Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid molecules of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

20 The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

25 According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

30 Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

25 In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

30 The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein.

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714 and 716. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOS

30	398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,
35	

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

20 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

30 (d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;

10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,

(d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or for the prevention of apoptosis in certain diseases, used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

25 The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as proteins, polysaccharides, polyalactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions. When a vaccine is used for protecting individuals against certain infections or diseases, it is called a prophylactic vaccine. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi or capable of treating proliferative disorders.

Also encompassed within the present invention are antibodies, monoclonal or polyclonal, capable of specifically binding to one or more epitopes of the polypeptides or proteins of the invention. The polypeptides of the invention are represented in SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

The term "specific binding" implies that there is substantially no cross-reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to techniques which are known to those skilled in the art. Monoclonal antibodies may be prepared using conventional hybridoma technology as described by Kohler and Milstein (1979). Polyclonal antibodies may also be prepared using conventional technology well known to those skilled in the art, and which comprises inoculating a host animal, such as a mouse, with a protein or epitope according to the invention and recovering the immune serum. The present invention also includes fragments of whole antibodies which maintain their binding activity, such as for example, Fv, F(ab') and F(ab')₂ fragments as well as single chain antibodies.

The antibodies of the invention are capable of specifically binding to at least one of the yeast or candida polypeptides as defined earlier or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue. The invention also relates to the use of said antibodies in treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases. Said antibodies may also be used for the preparation of a medicament for and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

Antibodies according to the invention may also be used in a method of detecting the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi where the yeast or fungus is chosen from, but not restricted to *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botrytis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response. According to another embodiment, the present invention provides a method of identifying compounds or polypeptides which selectively inhibit, induce or interfere with the

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

Another alternative to the above described method comprises (a) contacting a compound to be tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound. According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised.

Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion, detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell, optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the *GAL4* protein in yeast. *Gal4* is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of *Gal4*. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of *Gal4*. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a *GAL4* transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

10 All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

10 These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient thereof.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

15 According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

25 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30 According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable pharmaceutically acceptable carrier.

15 The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

20 Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic bax gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic

BAX-gene for expression in *Candida* spp. selected from the group of:

- 25 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
- b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
- c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
- d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90% or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as
- 30 defined in b) or c), and
- e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences.

or a nucleic acid representing the complement of any of said nucleic acids as defined in (e) to (d).

The synthetic BAX gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used *Candida* spp. codons, are used instead of the choice made for the sequence represented in

5 SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

15 As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic BAX, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic BAX gene and its fusion partner.

20 The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the invention is a *Candida* spp. cell.

25 In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic BAX gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic BAX gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID

5 NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

10 **YGL080W** (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (330 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

15 **YGR243W** (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

20 **YGR183C** (**QCR9**) (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

25 **YBR009C** (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

30 **Figure 3.** Yeast genome microarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

35 **Figure 4.** Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

5 **Figure 5.** Scheme for the synthesis of the synthetic BAX gene using *C. albicans* optimal codons.

Figure 6. DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans* BAX gene.

10 **Figure 7.** Representation of the expression constructs of the synthetic CaBAX gene (A) and the YEGFP-synth CaBAX fusion (B).

Figure 8. Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synthCaBAX and pGAL1P:GFP-synthCaBAX were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.

15 **Figure 9.** Growth kinetics of GAL1P:synthCaBAX (A) and GAL1P:GFP-synthCaBAX (B) on galactose containing minimal medium.

20 **Figure 10.** Immunoblot analysis of two independent transformants of GAL1P:synthCaBAX after 15 hours Bax induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the Bax protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal Bax antibody could be removed by the treatment with *S. cerevisiae* mannan.

Figure 11. Immunoblot analysis of the GAL1P:GFP-synthCaBAX strain on galactose containing minimal medium. The band appearing at 45kDa represents the Gfp-Bax fusion protein, while the band at 20kDa represents the Gfp protein alone.

25 **Figure 12.** FACS analysis of two independent GAL1P:GFP-synthCaBAX transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the GFP-fluorescence peak is not shaded.

30 **Figure 13.** Viability test synthCaBAX (A) and GFP-synthCaBAX transformants (B). Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.

35 **Table 1.** Oligonucleotides used for construction of the synthetic CaBAXx gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.

Tables 2-6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qi values were calculated using the Pathways™ software (Research Genetics).

Table 7. Genes modulated by Bax expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qi values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

Table 8. Codon usage for the synthetic BAX gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with YipUTyL or YipUTyLMuBax, after linearisation in the Ty

10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse bax cDNA, encoding the mouse Bax-α protein, was cloned by Pfu DNA polymerase (Stratagene®, La Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15 5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and
5'-TCAGCCCCATCTCTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20

Plasmid constructions

The 2μ ori and the *URA3* marker gene were removed from pUT332 (Gaignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI FLP* terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YipUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YipUT resulted in the plasmid YipUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-opened and blunted YipUTy resulted in the plasmid YipUTyL.

Mouse bax cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned into the *XbaI-HindIII*-opened plasmid YipUTyL, obtaining the final expression plasmid YipUTyLMuBax.

The plasmid YipUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA). The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results

Induction of Bax-expression in yeast cells

A preculture of yeast strain INVSc1 containing YipUTyLMuBax, wherein 5 Bax cassettes under the control of the *GAL1* promoter are integrated in the genome near *Ty* δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YipUTyL as a control. The precultures were diluted in 100-ml minimal glucose-containing medium and grown until an OD_{600} of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNeasy™ Reagent (GenHunter Corporation Nashville, TN, USA) according to the GenHunter protocol. $1.5 \cdot 10^8$ cells were concentrated in a microfuge tube and 1ml RNeasy™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 μ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 μ l RNase free dH_2O .

First strand cDNA synthesis in the presence of $\alpha^{32}P$ dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YipUTyLMuBax or INVSc1 YipUTyL yeast cells and incorporation of $\alpha^{32}P$ dCTP as follows: 2 μ l (1 μ g/ml) of Oligo dT was added to 20 μ g of total RNA in a maximal volume of 8 μ l RNase-free dH_2O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 μ l 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
- 1 μ l 0.1 M DTT
- 1 μ l RNase Block (40 units/ μ l) (Stratagene)
- 1.5 μ l 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
- 1.5 μ l SuperScript™ Reverse Transcriptase (200 units/ μ l) (GIBCO-BRL)
- 10 μ l $\alpha^{32}P$ dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala, Sweden).

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place. Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was $5 \cdot 10^8$ cpm/ μ g for both the INVSc1 YipUTyL and the INVSc1 YipUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³²P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0.5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 μ m using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2: Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H₂O₂-induced cell death

The oxidative H₂O₂-challenge

A preculture of yeast strain INVSc1 containing YipUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³²P dCTP

RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YipUTyL-MuBax or INVSc1 YipUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YipUTyL yeast cells. The specific activity of all probes was 5.10⁸ cpm/ μ g.

Quantification of Hybridisation Signals

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics, Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

Pairwise comparisons of the normalised data obtained from INVSc1 YipUTyL-MuBax (B) and INVSc1 YipUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (replacement).

Identification of Bax-specific genes within the Bax-responsive pool

Pairwise comparisons of the normalised data obtained from INVSc1 YipUTyL-MuBax (B) and INVSc1 YipUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YipUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathtoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA). Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix. The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell. Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 μ l minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent, flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 μ l of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAL-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAL-4, the medium is always supplemented with 20 $\mu\text{g/ml}$ uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (\pm 0.04) is reached.

200 μ l of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours. Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YipUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Eco*136II-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression In Candida cells

Strains

The *Candida albicans* strain CA14 (*ura3 Δ*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (*F'* *mcrA* Δ *mrr-hsdRMS-mcrBC*) \approx 80*lacZ* Δ M15 Δ *lacX74* *deoR* *recA1* *araD139* Δ *(ara-leu)*7697 *galJ* *galK* *rpsL* (*Str*^r) *endA1* *nupG*).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CA14), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic BAX gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised BAX gene

Construction of the synthetic BAX gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic BAX gene.

The synthCaBAX gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst*I site and a *Bgl*II site. The *Pst*I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl*II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma*I site, suitable for cloning into the expression vector.

Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.

Subsequently, fragment A was digested with *Pst*I and *Taq*I, fragment B with *Taq*I and *Bam*HI and fragment C with *Bam*HI and *Sma*I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst*I and *Sma*I resulting in the plasmid pUC21::synthCandidaBAX. The sequence of the synthetic BAX gene is shown in Figure 6.

Construction of synthetic BAX- and GFP-synthetic BAX expression plasmids

A *Pst*I-*Sma*I fragment containing the ORF of the synthetic BAX gene was cloned into the *Pst*I-*Sma*I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in the expression construct pGAL1P::synthCaBAX (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.

The yeast enhanced GFP gene *yEGFP*, (Cormack *et al.* 1997) was amplified by PCR using primer 5'-AACTGCAGATGCTCTAAAGGTGAAGAAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTCTCCITTTGTACAAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *YEGFP* gene into the PCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

The *YEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*-*Bgl*II *YEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Slu* I digested expression vector *pgAL1ACT1LUC*. The obtained *pgAL1P::YEGFP-synthCaBAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 Creation of the synthetic *BAX* expression strains

Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.* 1992). The plasmids were linearised with *Bpu*1102 I to allow directed integration into the genome at the *GAL*1 promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different transformants was prepared using the Nucleon® extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the *pgAL1P-synthCaBAX* plasmid as template, together with the sense primer 5'-ATGGATGGTCTGTGTAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCAATTTTTCACAGATG-3' (SEQ ID NO 14). Standard PCR conditions were used. For detection of the *YEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25 Western blot analysis

For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were prepared as described before (Sambook, Fritsch *et al.* 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.* 1999). Detection of the *Gfp* protein was done using an anti-*Gfp* monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD_{600} of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in microtitre plates using the Bioscreen C system (LabSystems).

5 Viability tests

Cells were pregrown in minimal dextrose medium to an OD_{600} of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse *Bax* protein was placed under control of the *Candida albicans* *GAL*1 promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the *YEGFP* to allow screening for transformants with a high *YEGFP*-synthCaBAX expression level using FACS technology. The newly obtained plasmids *pgAL1P::synthCaBAX* and *pgAL1::GFP-synthCaBAX* were transformed into the *C. albicans* CA14 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the *GAL*1 promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently, cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

Sequence 5' → 3'	
A1	TAAGAGCATCTTGTGTTGTTGTTCCAAAGGTCAATCTGGGGTTCCAGCC
A2	ATCTACCGCTCTATCTTGGATGAAACCTTGGCAACAAAGAACACC
A3	GGAATTCGACATCAGCATCTTGGCAATTCGAAATTCGAAATTCGAAATTC
A3	ATCACCGAATTCCTTCTCAACATTCAGACAAATTTTGGTAGAAGCATCTTG
A3	ID NO 5)
B1	GGAATTCGCTGATGTCGATACCGAATTCCTCAAGAGAGATCTTCTTCAAGT
B2	CTGCTGATATGTTGCTGATGTTGATGTTCACTTCAACTG (SED ID NO 6)
B2	AATCTGGGACCTTGGTACACAAAGCTTTCAGAACCAATTTAGAACCGCAAGTA
B3	GAAACAAAGGACGACCTTACCCAGTTGAAGTTACCA (SED ID NO 7)
B3	CCACCTTGATCTTGGATCCAGACCAACCAATCTTCTCTCAAGAAATTCAGAGTC
C1	CAACCCATGATGGTTCTGATCAATTCCTGGGACCTTG (SED ID NO 8)
C1	ATTGTTGGTCTGGATCCAGATCAAGGTGGTGGAAAGGTTTGTTGTTACTT
C2	CGGTACCCCAACCTGGGCAAAACCGTCA (SED ID NO 9)
C2	TCCCGGCGGGGATTAACCCATTTTTTCCAGATGGTCAAGAGCGGCTCAAGAC
C2	ACCAAGCAAGAGATGGTGACCGGTTTGGCCAGGTTGGG (SED ID NO 10)

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YIPUTL versus INVSc1 YIPUTLB**

Cellular role: Cell cycle control			
YBR133C	HSI7	18932.54	37877.20
YOR233C	MET32	17661.13	45567.17
YBR112C	SSN6	26698.87	65315.83
YOR145W	TAF61	38697.96	73117.62
YBR269W	SNF5	33111.77	72328.70
YBR216W	ADR1	30127.45	8615.87
YEL009C	GCN4	16533.78	3030.44
YBR089C-A	NHP6B	22698.93	6297.49
YMR043W	MCN1	39141.64	84180.45
YKR092C	SRP40	5965.83	16105.82
YMR273C	ZDS1	14899.61	35508.04
YPL089C	RLM1	34922.81	67856.88
YOR372C	NDI1	20285.12	44445.20
YPL037C	EGD1	30633.33	6250.70
Cellular role: Cell polarity			
YBL065W	BOI1	7693.28	18614.99
Cellular role: Chromatin structure			
YBR009C	HHF1	18668.00	4178.80
YNL003W	HHF2	48878.04	12568.96
YDR224C	HTB1	67355.40	23156.82
YBL002W	HTB2	25269.02	5383.97
Cellular role: RNA processing			
YER112W	US51	12776.74	31470.70
YPL090C	NAB3	6381.36	17892.11
YNL112W	DBP2	9956.84	28036.48
Cellular role: Energy generation			
YPL078C	ATP4	28902.68	5980.38
YDL004W	ATP16	35525.08	3004.34
YDR037W	ATP17	14419.41	758.86
YDR529C	QCH7	35346.95	5394.65
YGR008C	SIF2	13275.51	2276.27
YEL039C	CYC7	13604.38	2889.86
YKL150W	MCRI	10537.67	30743.75
YLR088C	COX12	52987.73	5455.83
YLR327C		113.966.77	54.014.65
Cellular role: Carbohydrate metabolism			
YBR149W	ARA1	15149.55	4095.17
YHR094C	HXT1	12526.90	785.73
YDR343C	HXT3	36643.13	1632.48
YDR343C	HXT6	77064.71	32060.05
YDR342C	HXT7	76349.13	27615.15
Cellular role: Signal transduction			
YER117W	BMH1	22856.29	44771.71
YDR099W	BMH2	40127.38	74572.38

YGR070W	ROM1	12055.28	28169.57	↑	2.34
YGR023W	MTL1	7354.78	19848.06	↑	2.67
Cellular role: Protein synthesis					
YGR034W	RPL26B	71942.48	74825.22	↑	1.04
Cellular role: Protein folding					
YLR216C	CPH6	9616.80	31128.02	↑	3.24
Cellular role: Protein modification/degradation					
YFR052W	RPN12	5383.57	14855.67	↑	2.66
YDL147W	RPN5	31932.20	52939.11	↑	1.86
YGR132C	PHB1	15428.56	5591.19	↓	2.76
YGR135W	PRE8	39921.63	5517.17	↓	7.24
YFR010W	UBP8	1882.76	828.84	↓	2.28
Cellular role: Cell stress					
YHR037W	GPX3	7868.22	21789.00	↑	2.77
YDR513W	TRT1	55986.32	33263.12	↓	1.89
YCL035C	GRX1	70248.30	10899.97	↓	6.40
YEL014W	HSP12	41689.29	18658.48	↓	2.23
YHR053C	CUP1A	72852.07	43488.52	↓	1.88
YHR055C	CUP1B	71834.03	56799.80	↓	2.77
YMR173W	DDR48	16670.70	5022.40	↓	3.32
YMR51W-A	HOR7	26876.95	417.36	↓	64.41
YLR043C	TRX1	58251.39	4455.79	↓	13.13
YBL064C	PRX1	21525.00	40865.00	↑	1.80
YOL151W	GRE2	2824.55	24152.03	↑	9.20
Cellular role: Unknown					
YBL081W		73834.11	74612.35	↑	1.01
YDR366C		39998.46	57428.80	↑	1.44
YCR004C	YCP4	6869.06	28115.73	↑	4.09
YBR013C		3988.55	15144.34	↑	3.80
YBR050C	REG2	4687.91	14408.20	↑	3.07
YBL100W		18744.60	35440.24	↑	1.89
YDR154C		19565.23	68428.03	↑	3.55
YEL071W	DLD3	22235.73	68790.83	↑	3.09
YHR065W		14426.76	34898.68	↑	2.42
YGR069W		43413.57	72420.39	↑	1.67
YDR544C		13567.00	27004.37	↑	1.99
YGR236C		24927.59	8032.35	↓	3.10
YIL057C		24246.39	773.56	↓	31.34
YGL080W		23425.00	3217.81	↓	7.28
YGL072C		18437.52	2662.80	↓	6.20
YHR066C	RSC30	72072.88	57446.85	↓	1.25
YKL054C	VID31	17990.49	38259.80	↑	2.13
YLR311C		7892.40	24164.87	↑	3.02
YJRI15W		64690.69	102066.34	↑	1.58
YJL188C	BUD19	7580.28	22325.70	↑	2.95
YKR040C		50934.78	100733.41	↑	1.98
YLR053C		8117.66	20317.34	↑	2.50
YOR121C		59950.94	92470.43	↑	1.54
YNL143C		98811.28	110534.34	↑	1.12
YOR131C		7841.55	22353.72	↑	2.81
YNL38W		21800.45	38177.28	↑	1.78
YNL179C		13729.36	39516.53	↑	2.88
YOL150C		3408.74	60298.39	↑	17.89

YMR107W	65118.70	10042.46	↓	6.48	
YKL065C	YET1	89556.19	12804.88	↓	5.43
YJR096W		21780.37	10655.13	↓	2.04
YJL161W		16488.73	2618.26	↓	6.29
YML128C	MSC1	80130.20	13795.84	↓	5.81
YMR251W		28879.95	417.38	↓	64.41
YMR173W-A		110104.98	61851.23	↓	1.78
YPL201C		17913.32	5018.97	↓	3.57
YOR265W		64074.73	29749.43	↓	2.15
YOR266W		13458.08	733.08	↓	18.36
Cellular role: Cell wall maintenance					
YKR076W	ECM4	2674.15	13040.04	↑	4.88
YLR390W	ECM19	5472.05	15145.85	↑	2.77
Cellular role: Membrane fusion					
YHR138C		18921.35	3707.57	↓	5.37
Cellular role: Vesicular transport					
YHR161C	YAP180A	13086.35	30160.90	↑	2.30
YPL065W	SEC16	6868.57	15208.49	↑	2.28
YKL196C	YKT6	18933.84	2890.07	↓	6.55
YPR029W	YIP2	25434.34	2049.47	↓	12.41
Cellular role: DNA repair/recombination					
YDL059C	RAD59	1948.61	13089.13	↑	6.72
Cellular role: DNA synthesis					
YEL032W	MCN3	23422.85	44327.48	↑	1.89
Cellular role: Amino acid metabolism					
YIL074C	SER33	3978.42	16702.66	↑	4.20
YGR155W	CYS4	4184.59	19270.89	↑	4.61
Cellular role: Fatty acid metabolism					
YHR179W	OYE2	2291.36	40274.02	↑	17.58
Cellular role: Protein translocation					
YNL131W	TOM22	16287.21	1679.78	↓	9.70
Cellular role: Small molecule transport					
YDR276C	SNA1	21148.46	1580.68	↓	13.38
YOR267C	HRK1	62689.30	110516.24	↑	1.76
YHR039-C	VMA10	60107.90	8490.93	↓	7.08
YOR382W	FIT2	6780.82	27236.15	↑	4.02

Table 3: Overview of the differentially expressed genes after 1h Box expression
Comparison: INVSc1 YipUTL versus INVSc1 YipUTyLB

Gene	Gene	Normalized expression	log2 fold change	P-value	
Cellular role : Polymerase II transcription					
YDR145W	TAF61	20729.58	57376.27	↑	2.77
YDR216W	ADR1	5925.91	18459.00	↑	3.11
YHR112C	CYC8	50188.77	84511.50	↑	1.29
YMR043W	MCM1	21011.54	53700.49	↑	2.56
YPL089C	RLM1	23440.54	84284.32	↑	2.74
YOR372C	NDI1	28412.58	50804.99	↑	1.92
Cellular role : Cell cycle control					
YBR139C	HSL7	18761.64	53238.86	↑	2.84
Cellular role : Cell polarity					
YBL085W	BOJ1	37895.40	57761.52	↑	1.52
Cellular role : Chromatin structure					
YDR224C	HTB1	13681.40	55656.34	↑	4.07
Cellular role : Energy generation					
YGR183C	QCR9	23181.54	81865.40	↑	3.53
YLR294C	MCR1	5054.57	28994.72	↑	5.74
YKL150W	MCF1	43863.07	60593.16	↑	1.39
YMR256C	COX7	7606.58	28801.54	↑	3.79
YOL126C	MDH2	34144.81	65326.97	↑	1.81
YLR327C		97415.94	101651.17	↑	1.04
Cellular role : Vesicular transport					
YHR161C	YAP180A	11602.81	34695.20	↑	2.89
YLR206W	ENT2	14439.24	34621.70	↑	2.40
Cellular role : Carbohydrate metabolism					
YDR342C	HXT7	65273.56	22231.06	↓	2.94
YDR343C	HXT6	43572.28	6075.38	↓	7.17
YDR345C	HXT3	76352.52	40298.00	↓	1.89
YGR192C	TDH3	38472.30	14145.84	↓	2.72
YKR097W	PCK1	22819.81	38225.98	↑	1.67
YOR374W	ALD4	33711.37	2607.43	↓	12.83
Cellular role : Signal transduction					
YER177W	BMH1	16298.14	31748.91	↑	1.95
YDR099W	BMH2	50572.45	65123.58	↑	1.29
Cellular role : Cell wall maintenance					
YLR110C	CCW12	102525.29	11230.41	↓	9.13
Cellular role : Protein modification/degradation					
YOR261C	RPN8	12575.49	32568.47	↑	2.59
Cellular role : Cell stress					
YHR055C	CUP1A	32531.53	83579.94	↑	1.95
YHR055C	CUP1B	27839.92	65142.82	↑	2.33
YMR173W	DDR48	38338.83	60514.70	↑	1.58
YOR031W	CRS5	2922.32	23848.80	↑	8.16

YLR109W	AHP1	43067.08	6302.46	↓	6.53
Cellular role: Unknown					
YBL081W		82476.13	44279.86	↑	1.86
YBL109W		22998.63	63428.23	↑	2.76
YDR366C		14599.17	46494.73	↑	3.18
YDR154C		21266.57	56534.93	↑	2.65
YGR236C	SPG1	17717.80	64439.96	↑	3.64
YHR066C	RSC30	27020.16	65110.42	↑	2.41
YGR182C		8171.02	34669.96	↑	4.24
YDR544C		14797.70	37704.91	↑	2.55
YHR162W		13836.79	33381.64	↑	2.41
YGR296C		30829.66	59765.39	↑	1.94
YGR243W		14008.24	29603.16	↑	2.11
YHR050C	PEG2	19467.41	35273.39	↑	1.81
YEL071W	DLD3	83074.54	62988.96	↓	1.32
YDR133C		83111.03	16839.53	↓	4.94
YDR134C		46028.06	8577.00	↓	5.37
YHL021C		28018.46	66537.91	↑	2.37
YKL054C	VID31	7803.52	31160.73	↑	3.99
YLR311C		13453.15	78850.98	↑	5.86
YHR107W		6751.84	24129.32	↑	2.76
YKL066W		38338.83	60514.70	↑	1.58
YHR173W-A		23670.86	66254.48	↑	2.80
YML053C		17039.58	58016.58	↑	3.40
YOR121C		19817.67	69853.66	↑	3.51
YOL106W		17864.90	49911.08	↑	2.79
YML338W		84658.02	98161.71	↑	1.16
YJRI15W					
Cellular role: Small molecule transport					
YOR267C	HFK1	90123.84	86824.51	↑	1.07

Table 4: Overview of the differentially expressed genes after 2h Bax expression
Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

		Cellular role: Protein modification/degradation			
YCL052C	PBN1	5284.22	815.70	↑	1.55
YDL147W	RPN5	22386.40	47857.67	↑	2.14
YOR261C	RPN6	27349.25	42198.05	↑	1.54
YGR132C	PHB1	5252.03	8459.53	↑	1.61
YBR139W		9458.26	3611.21	↓	2.62
		Cellular role: Unknown			
YDR202C	PAV2	7483.71	10089.19	↑	1.35
YBR082C		4893.97	9898.82	↑	2.02
YDR366C		25468.2	59682.82	↑	2.34
YBL109W		24803.62	37444.64	↑	1.51
YDR154C		21166.26	33434.35	↑	1.58
YEL071W	DLD3	34153.85	44083.39	↑	1.29
YGR236C	SPG1	16978.52	31419.12	↑	1.85
YGR182C		30569.31	56805.05	↑	1.92
YDR544C		15637.14	24421.99	↑	1.53
YHR162W		28610.34	33794.73	↑	1.27
YHR056C	RSC30	33372.66	68425.24	↑	2.05
YDR133C		73520.99	82984.59	↑	1.20
YDR134C	ADY2	17240.59	11835.82	↓	1.46
YCH010C		72723.66	53767.35	↓	1.22
YGR069W		65418.73	2198.04	↓	7.44
YIL057C		16510.16	6509.91	↓	1.88
YGL072C		12209.88	11525.24	↓	1.96
YGL080W		22560.76	24680.47	↑	2.22
YLR311C		11095.31	103422.48	↑	1.38
YJRI15W		74767.79	11477.42	↑	1.63
YMR099C		7057.15	48886.91	↑	1.47
YMR173W-A		31901.05	34695.33	↑	1.42
YML132W	COO3	24648.97	25433.87	↑	1.87
YKL066W		13561.84	11920.21	↑	1.85
YIL142C		7205.86	11569.83	↑	1.79
YLR546C		8447.57	78638.82	↑	1.91
YLR053C		41161.10	28681.23	↑	1.53
YMR110C		19410.64	28948.72	↑	1.57
YKR075C		19104.57	59462.09	↑	1.53
YOR121C		38492.56		↑	

		Cellular role : Unknown			
YOL106W		31382.10	76684.72	↑	2.44
YNL339W		24117.93	38981.22	↑	1.62
YNL134C		9817.33	14813.60	↑	1.52
YKL065C	YET1	52422.65	33794.03	↓	1.55
YMR009W		20868.22	9519.29	↓	2.17
YLL144W		10316.92	3122.77	↓	3.30
YNL128C	MSC1	584128.13	25434.11	↓	2.29
YNL179C		21838.98	10883.88	↓	2.02
YOL109W	ZE01	22711.98	6581.11	↓	3.45
YNR002C	FUN34	18241.25	9752.25	↓	1.87
Cellular role : Chromatin structure					
YDR224C	HTB1	25356.73	30827.54	↑	1.22
YBL002W	HTB2	9241.68	14281.54	↑	1.54
YBL003C	HTA2	3453.55	6553.49	↑	1.90
YNL031C	HHT2	13376.02	2348.84	↓	5.69
Cellular role : Polymerase II transcription					
YBR269W	SNF5	59542.27	65885.13	↑	1.11
YDR073W	SNF11	12190.01	23088.03	↑	1.89
YMR043W	MCM1	68457.16	77022.05	↑	1.16
YPL089C	RLM1	49844.99	60624.28	↑	1.22
Cellular role : Signal transduction					
YDR069W	BMH2	55902.13	73874.51	↑	1.32
Cellular role : Cell stress					
YBL084C	PRX1	11203.87	14815.42	↑	1.32
YBR101C		25016.27	35781.64	↑	1.43
YLR043C	TRX1	10864.53	3912.03	↓	2.78
YGR209C	TRX2	30492.33	37829.20	↑	1.24
YER103W	SSA4	8763.38	15799.18	↑	1.80
YHR055C	CUP1B	18824.43	77613.05	↑	4.12
YHR053C	CUP1A	32726.82	63536.72	↑	1.94
YDR256C	CTA1	9814.29	4232.17	↓	2.27
YCR021C	HSP30	8090.05	3604.78	↓	2.24
YCL035C	GRX1	28437.57	12843.99	↓	2.21
YGR086C		38706.12	24272.57	↓	1.52
YFL014W	HSP12	61868.64	23288.19	↓	2.66
YOR031W	CRS5	6015.69	14519.12	↑	2.41
YMR251W-A	HOR7	17731.14	4231.39	↓	4.19
YOR120W	GCY1	114252.98	78052.05	↓	1.46
Cellular role : Protein synthesis					
YAL003W	EFB1	3044.80	5772.68	↑	1.90
YOL127W	RPL25	6266.96	12055.41	↑	1.92
YHR010W	RPL27	4057.16	10856.34	↑	2.68
YLR325C	RPL38	5401.85	12955.89	↑	2.40
YLL189W	RPL39	2044.64	8010.67	↑	3.92
YLL148W	RPL40A	5052.35	11595.54	↑	2.30
YKR094C	RPL40B	3984.57	10011.13	↑	2.54
YOL139C	CDC33	4132.18	8958.14	↑	2.17

		Cellular role : Protein folding			
YLR216C	CPR8	20353.43	32713.37	↑	1.61
YKL177W	SBA1	11144.25	1500.56	↓	7.43
Cellular role : Vesicular transport					
YCR009C	RVS161	5350.32	9780.92	↑	1.83
YHR161C	YAP180A	25136.63	32481.67	↑	1.28
YBL076C	AUT7	16528.91	9843.25	↓	1.88
Cellular role : Carbohydrate metabolism					
YBL058W	SHP1	4626.50	8178.94	↑	1.77
YBR149W	APR1	30708.41	9837.76	↓	3.19
YDR178W	SDH4	14880.91	8237.35	↓	2.39
YHR094C	HXT1	30389.99	18383.00	↓	1.65
YMR011W	HXT2	39524.90	21221.96	↓	1.88
YDR345C	HXT3	77025.40	56749.40	↓	1.38
YDR343C	HXT6	73149.70	8678.17	↓	8.43
YDR342C	HXT7	75331.76	27052.43	↓	2.78
YKL060C	FBA1	16273.54	21323.23	↑	1.31
Cellular role : Cell cycle control					
YBR133C	HSL7	32903	41884.32	↑	1.28
Cellular role : Energy generation					
YMR256C	COX7	18558.01	40422.91	↑	2.18
YML129C	COX14	11418.54	21798.88	↑	1.91
YFR033C	QCR6	9159.48	13398.87	↑	1.48
YDR239C	QCR7	24821.75	16556.87	↓	1.50
YLL168W	QCR8	15554.30	24509.28	↑	1.58
YHR001W-A	QCR10	12418.35	23465.31	↑	1.68
YBR039W	ATP3	11709.79	3086.19	↓	3.78
YPL078C	ATP4	11325.84	13769.72	↑	1.22
YPL271W	ATP15	3261.75	7839.05	↑	2.40
YLR327C		51742.90	128511.27	↑	2.48
YLR294C		15832.81	38544.44	↑	2.43
YAL060W	FUN49	11792.72	5778.91	↓	2.04
Cellular role : Small molecule transport					
YDR276C	SNA1	19337.39	12392.29	↓	1.58
YGR197C	SNG1	4766.18	10484.09	↑	2.20
YHR039C-B	VMA10	21190.93	10592.88	↓	2.00
YOR267C	HRK1	111849.17	101339.10	↓	1.10
Cellular role : RNA processing					
YGR250C		8709.92	17358.43	↑	1.99
Cellular role : Cell wall maintenance					
YER150W	SPH1	55592.73	22403.59	↓	2.48
YLR110C	CCW12	35147.41	5786.88	↓	6.07
Cellular role : Cell polarity					
YOR122C	PPY1	14459.45	20176.41	↑	1.40
Cellular role : Amino acid metabolism					
YPR035W	GLN1	20894.14	7522.05	↓	2.78

Table 5: Overview of the differentially expressed genes after 3h Bax expression

Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

Gene	Gene	Normalised intensities	Log2	Log2	Log2
Cellular role : Cell cycle control					
YBR133C	HSL7	63582.10	43191.28	↓	1.47
Cellular role : Cell polarity					
YBL065W	BOI1	32734.79	23497.41	↓	1.39
Cellular role : Chromatine structure					
YDR545W	YRF1-1	20111.51	11479.67	↓	1.75
Cellular role : Energy generation					
YGR005C	CIT2	11882.42	25632.94	↓	2.16
YGR183C	OCR9	74474.20	11510.99	↓	6.47
YOL126C	MDH2	55984.88	17978.10	↓	3.11
Cellular role : Carbohydrate metabolism					
YBR019C	GAL10	3092.50	15697.54	↑	5.08
YDR345C	HXT3	14088.41	25657.68	↑	1.82
YKR097W	POK1	50736.44	20858.02	↓	2.43
Cellular role : Signal transduction					
YDR099W	BMH2	63285.16	56028.91	↓	1.13
Cellular role : Protein synthesis					
YHR010W	RPL27A	23254.90	7217.14	↓	3.22
YLR325C	RPL38	26725.96	9121.29	↓	2.93
Cellular role : Cell stress					
YFL014W	HSP12	40848.44	69781.91	↑	1.71
YHR053C	CUP1A	20399.10	65037.14	↑	3.19
YHR055C	CUP1B	21783.09	64594.59	↑	2.97
YMR173W	DDR48	75407.18	36354.37	↓	2.07
YOL052C-A	DDR2	20479.72	33702.23	↑	1.65
Cellular role : Unknown					
YIL057C		7802.78	24104.02	↑	3.17
YHR056C	RSC30	41473.41	64809.08	↑	1.56
YDR544C		55075.67	29731.72	↑	1.85
YKR040C		48049.71	59649.47	↑	1.24
YNL338W		86107.91	30045.62	↑	2.87
YLR115W		74889.58	81238.98	↑	1.08
YBL109W		64754.79	57185.99	↓	1.13
YMR173W-A		75407.16	36354.37	↓	2.07

Table 6: Overview of the differentially expressed genes after 6h Bax expression

Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

Gene	Gene	Normalised intensities	Log2	Log2	Log2
Cellular role : Cell stress					
YDR171W	HSP42	13484.04	27183.07	↑	2.02
YFL014W	HSP12	41197.12	29081.08	↑	1.42
YDR131W	THP1	19895.22	12935.62	↓	1.54
YCL035C	GRX1	31735.39	12930.71	↓	2.45
YGR209C	TRX2	54455.65	47569.21	↓	1.14
YHR053C	CUP1A	81488.84	15289.39	↓	5.33
YHR055C	CUP1B	81278.95	20031.69	↓	4.06
YMR251W-A	HOH7	18824.54	5914.28	↓	3.18
Cellular role : Signal transduction					
YDR099W	BMH2	28412.99	58598.42	↑	1.99
Cellular role : Protein synthesis					
YGL147C	RPL9A	13655.68	1585.97	↓	8.61
YGR085C	RPL11B	27465.15	3781.35	↓	7.24
YDR418W	RPL12B	14417.77	1555.24	↓	9.27
YLR029C	RPL15A	37122.11	9321.81	↓	3.98
YOR312C	RPL20B	50334.94	5708.59	↓	8.82
YBR191W	RPL21A	21740.90	2571.30	↓	8.46
YPL079W	RPL21B	31059.43	5023.61	↓	6.18
YOL127W	RPL25	75971.72	11749.17	↓	6.47
YHR010W	RPL27A	45716.64	8096.40	↓	5.65
YDR471W	RPL27B	14638.79	2813.40	↓	5.60
YOL075W	RPL31A	11969.47	2611.53	↓	4.58
YBL092W	RPL32	7872.80	857.85	↓	9.18
YDL191W	RPL35A	28582.59	6046.25	↓	4.73
YDL136W	RPL35B	25433.49	5084.51	↓	5.02
YLR325C	RPL38	48051.23	8217.18	↓	5.85
YHR148W	RPL40A	47028.95	9543.85	↓	4.93
YKR094C	RPL40B	39900.50	5957.78	↓	6.70
YHR141C	RPL42B	10163.88	937.21	↓	10.84
YML063W	RPS1B	15916.48	1144.54	↓	13.91
YGL123W	RPS2	12505.58	2243.26	↓	5.57
YOR096W	RPS7A	24164.37	3223.60	↓	7.50
YBL072C	RPS8A	17188.50	3233.30	↓	5.32
YER102W	RPS8B	16234.83	1791.18	↓	8.06
YBR189W	RPS9B	10075.22	2150.89	↓	4.88
YOR293W	RPS10A	51787.23	12110.74	↓	4.28
YDR064W	RPS13	9736.57	1587.67	↓	6.13
YDR450W	RPS18A	37813.71	5874.80	↓	6.86
YML026C	RPS19B	14458.01	2027.28	↓	7.13
YKL156W	RPS27A	23725.18	11117.26	↓	2.13
YLR167W	RPS31	38648.54	2611.97	↓	14.80
YIL138C	TIF2	20154.61	7264.86	↓	2.77
Cellular role : Energy metabolism					
YGR183C	OCR9	57357.59	80447.53	↑	1.40
YDL004W	ATP16	25047.95	10988.85	↑	2.28
YKL150W	MCRI	50931.46	37076.83	↑	1.37

YLR038C	COX12	39508.08	29534.70	↓	1.34
Cellular role: Unknown					
YDR442W		14854.81	2242.42	↓	6.54
YDR134C		17025.59	10561.72	↓	1.61
YHR056C	RSC30	81350.52	31447.10	↓	2.59
YKR040C		48390.21	90125.88	↑	1.86
YLR414C		13463.40	8085.92	↓	1.87
YLR312C		25589.67	16184.57	↓	1.58
YJL188C	BUD19	22074.09	4526.39	↓	4.88
YOR265W		75099.98	61898.00	↓	1.21
YOL109W	ZEO1	68287.15	35502.43	↓	1.87
Cellular role: Chromatine structure					
YBR009C	HMF1	11173.15	5416.74	↓	2.08
YNL030W	HMF2	31368.74	20132.23	↓	1.56
Cellular role: Nucleotide metabolism					
YDR399W	HPT1	13339.03	5333.81	↓	2.50
Cellular role: Polymerase II transcription					
YEL009C	GCN4	34617.98	20798.63	↓	1.66
YPL037C	EGD1	17882.37	8228.01	↓	2.17
Cellular role: Vesicular transport					
YBL078C	AUT7	42661.70	32333.01	↓	1.32
YOR327C	SNC2	22716.56	13704.48	↓	1.66
Cellular role: Small molecule transport					
YHR039C-B	VMA10	44429.30	23826.51	↓	1.86
Cellular role: Cell wall maintenance					
YKL097W-A	CWP2	13529.93	1617.20	↓	8.37
Cellular role: Carbohydrate metabolism					
YKL060C	FBA1	33329.74	10367.82	↓	3.21

Table 7:

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 17	YAL003W	EFB1			1.90		
SEQ ID NO 19	YAL060W	FUN49			-2.00		
SEQ ID NO 21	YBL002W	HTB2	-4.69		1.54		
SEQ ID NO 23	YBL058W	SHI1			1.77		
SEQ ID NO 25	YBL064C	PRX1	1.90		1.32		
SEQ ID NO 27	YBL072C	RPS8A					-5.32
SEQ ID NO 29	YBL081W	BOI1	1.01	1.88			
SEQ ID NO 31	YBL085W	RPL32	2.42	1.52		-1.39	
SEQ ID NO 33	YBL092W		1.89	2.76	2.76	-1.13	-8.18
SEQ ID NO 35	YBL109W	HMF1	-3.89		1.51		
SEQ ID NO 37	YBR009C	GAL10				5.08	-2.08
SEQ ID NO 39	YBR019C	ATP3			-3.70		
SEQ ID NO 41	YBR039W	REG2	3.07	2.11	2.02		
SEQ ID NO 43	YBR050C						
SEQ ID NO 45	YBR062C						
SEQ ID NO 47	YBR089C-A	NHP88	-3.60		1.43		
SEQ ID NO 49	YBR101C						
SEQ ID NO 51	YBR112C	SSN6	2.45	1.28	1.28	-1.47	-4.68
SEQ ID NO 53	YBR133C	HSL7	2.00	2.84	-2.60		-8.46
SEQ ID NO 55	YBR139W				-3.11		
SEQ ID NO 57	YBR149W	APA1	-3.70				
SEQ ID NO 59	YBR169W	RPS8B				2.16	
SEQ ID NO 61	YBR191W	RPL21A					
SEQ ID NO 63	YBR289W	SNF5	2.18		1.11		
SEQ ID NO 65	YCL035C	GRX1	-8.40		-2.20		-2.45
SEQ ID NO 67	YCL052C	PBN1			1.55		
SEQ ID NO 69	YCR004C	YCP4	4.09				
SEQ ID NO 71	YCR005C	CIT2			1.83		
SEQ ID NO 73	YCR009C	RVS181			-1.40		
SEQ ID NO 75	YCR010C						
SEQ ID NO 77	YCR013C		3.80		-2.20		
SEQ ID NO 79	YCR021C	HSP30					-2.28
SEQ ID NO 81	YDL004W	ATP16	-12.16				
SEQ ID NO 83	YDL059C	RAO59	6.72				-4.58
SEQ ID NO 85	YDL075W	RPL31A			2.14		
SEQ ID NO 87	YDL147W	RPN5	1.66				-6.13
SEQ ID NO 89	YDR064W	RPS13					
SEQ ID NO 91	YDR073W	SNF11	1.86		1.89	-1.13	1.99
SEQ ID NO 93	YDR099W	BMH2		1.29	1.32		
SEQ ID NO 95	YDR133C			-1.32	-1.20		-1.61
SEQ ID NO 97	YDR134C			-4.94	-7.40		
SEQ ID NO 99	YDR145W	TAF61	1.89	2.77			
SEQ ID NO 101	YDR154C		3.55	2.85	1.58		2.02
SEQ ID NO 103	YDR171W	HSP42					
SEQ ID NO 105	YDR178W	SDH4			-2.30		
SEQ ID NO 107	YDR202C	RAV2			1.35		
SEQ ID NO 109	YDR216W	ADR1	-3.42	3.11			
SEQ ID NO 111	YDR224C	HTB1	-2.91	4.07	1.22		
SEQ ID NO 113	YDR253C	MET32	2.58				
SEQ ID NO 115	YDR256C	CTA1			-2.20		
SEQ ID NO 117	YDR276C	SNA1	-13.38		-1.50		

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 118	YDR342C	HXT7	-2.76	-2.94	-2.70		
SEQ ID NO 121	YDR343C	HXT6	-2.40	-7.17	-8.40		
SEQ ID NO 123	YDR345C	HXT3	-22.45	-1.89	-1.30	1.82	
SEQ ID NO 125	YDR366C		1.44	3.18	2.34		
SEQ ID NO 127	YDR377W	ATP17	-18.05				-2.50
SEQ ID NO 129	YDR399W	HP11					-9.27
SEQ ID NO 131	YDR418W	RPL12B					-1.54
SEQ ID NO 133	YDR513W	TR1	-1.68		1.53	-1.85	
SEQ ID NO 135	YDR544C		1.99	2.55		-1.75	-1.66
SEQ ID NO 137	YDR545W	YRF1.1					
SEQ ID NO 139	YEL009C	GCN4	-5.46				
SEQ ID NO 141	YEL032W	MCN3	1.89				
SEQ ID NO 143	YEL039C	CYC7	-5.06				
SEQ ID NO 145	YEL071W	DLD3	3.09	1.81	1.29		
SEQ ID NO 147	YER103W	SSA4			1.80		
SEQ ID NO 149	YER112W	US51	2.46		-2.40		
SEQ ID NO 151	YER150W	SP1	1.98	1.95			
SEQ ID NO 153	YFR010W	UBP6	-2.28		1.46		
SEQ ID NO 155	YFR033C	OCR6	2.66				
SEQ ID NO 157	YFR052W	RPV12	-6.20		-1.80		-5.57
SEQ ID NO 159	YGL072C		-7.28		-1.90		
SEQ ID NO 161	YGL123W	RP52					
SEQ ID NO 163	YGR028C	STR2	-5.83				
SEQ ID NO 165	YGR023W	MTL1	2.87				
SEQ ID NO 167	YGR034W	RPL26B	1.04		-1.20		
SEQ ID NO 169	YGR069W	ROM1	1.67		-1.50		
SEQ ID NO 171	YGR070W		2.34		-1.81		
SEQ ID NO 173	YGR086C						
SEQ ID NO 175	YGR132C	PHB1	-2.76				
SEQ ID NO 177	YGR135W	PRE9	-7.24				
SEQ ID NO 179	YGR155W	CYS4	4.61				
SEQ ID NO 181	YGR192C	TDH3		-2.72	2.20		
SEQ ID NO 183	YGR197C	SNG1			1.24		-1.14
SEQ ID NO 185	YGR209C	TRX2					
SEQ ID NO 187	YGR243W			1.94	1.99		
SEQ ID NO 189	YGR250C						
SEQ ID NO 191	YHL021C			-5.37	1.89		
SEQ ID NO 193	YHR001W-A	OCR10			-2.00		-1.86
SEQ ID NO 195	YHR039C-B	VMA10	-7.08		1.94	3.19	-5.33
SEQ ID NO 197	YHR053C	CUP1A	-1.88	1.95	1.94	2.97	-4.06
SEQ ID NO 199	YHR055C	CUP1B	-2.77	2.33	4.12	1.56	-2.59
SEQ ID NO 201	YHR056C		-1.25	2.41	2.05		
SEQ ID NO 203	YHR094C	HXT1	-15.94		-1.60		
SEQ ID NO 205	YHR095W		2.42				
SEQ ID NO 207	YHR136C	YAP180A	-5.37	2.99	1.29		
SEQ ID NO 209	YHR161C		2.30	2.41	1.27		
SEQ ID NO 211	YHR162W						
SEQ ID NO 213	YHR179W	OVE2	17.58		-7.50	3.17	
SEQ ID NO 215	YIL057C	SER33	-31.34				
SEQ ID NO 217	YIL074C		4.20				
SEQ ID NO 219	YIR037W	GPX3	2.77				

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	6h
SEQ ID NO 223	YIL138C	TRF2			1.65		-2.77
SEQ ID NO 225	YIL142C				-3.30		
SEQ ID NO 227	YIL144W		-6.29		1.58		
SEQ ID NO 229	YIL161W						
SEQ ID NO 231	YIL166W	OCR8	-2.04	1.16	1.38	-1.08	
SEQ ID NO 233	YJR096W		1.58	2.37	1.31		-3.21
SEQ ID NO 235	YJR115W	VLD31	2.13		-1.55		
SEQ ID NO 237	YKL054C	FBA1			1.87		
SEQ ID NO 239	YKL080C	YET1	-5.43	2.76			
SEQ ID NO 241	YKL085C						
SEQ ID NO 243	YKL068W						
SEQ ID NO 245	YKL097W-A	CWP2			-7.43		-8.37
SEQ ID NO 247	YKL117W	SB1	-3.43	1.39			-1.37
SEQ ID NO 249	YKL150W	MCRI					-2.13
SEQ ID NO 251	YKL156W	RP527A	-6.55			1.24	1.86
SEQ ID NO 253	YKL196C	YKT6	1.98		1.57		
SEQ ID NO 255	YKR040C						
SEQ ID NO 257	YKR075W	ECM4	4.88				
SEQ ID NO 259	YKR092C	SRP40	2.70	1.67		-2.43	-3.98
SEQ ID NO 261	YKR097W	PCK1					-1.34
SEQ ID NO 263	YLR029C	RPL15A	-9.66		-2.78		
SEQ ID NO 265	YLR038C	COX12	-13.13		1.91		
SEQ ID NO 267	YLR043C	TRX1	2.50	-6.83	-6.07		
SEQ ID NO 269	YLR053C			2.40	1.61		
SEQ ID NO 271	YLR109W	AHP1		5.74	2.43		
SEQ ID NO 273	YLR110C	ENT2	3.24	3.99	2.22		
SEQ ID NO 275	YLR206W	CPH6					
SEQ ID NO 277	YLR216C		3.02				
SEQ ID NO 279	YLR294C		-2.10	1.04	2.48		-1.58
SEQ ID NO 281	YLR311C				1.79		
SEQ ID NO 283	YLR312C						
SEQ ID NO 285	YLR327C						
SEQ ID NO 287	YLR346C	ECM19	2.77	2.80			-1.67
SEQ ID NO 289	YLR390W						
SEQ ID NO 291	YLR414C						
SEQ ID NO 293	YML053C	COX14			1.91		
SEQ ID NO 295	YML129C	COX3			-2.17		
SEQ ID NO 297	YML129W				-1.86		
SEQ ID NO 299	YMR009W	HXT2	2.15	2.56	1.16		
SEQ ID NO 301	YMR011W	MCMI			1.63		
SEQ ID NO 303	YMR043W		-6.48	5.86	1.53		
SEQ ID NO 305	YMR099C						
SEQ ID NO 307	YMR107W		-3.32	1.58	1.47	-2.07	
SEQ ID NO 309	YMR110C		-64.41				
SEQ ID NO 311	YMR173W-A	DDR48	-1.78	1.58			
SEQ ID NO 313	YMR251W-A		-64.41		-4.19		-3.18
SEQ ID NO 315	YMR251W						
SEQ ID NO 317	YMR256C	HOR7	-64.41	3.79	2.18		
SEQ ID NO 319	YMR273C	COX7	2.42				
SEQ ID NO 321	YML030W	ZDS1	-3.97				
SEQ ID NO 323	YML031C	HHP2					
SEQ ID NO 325		HHT2			-5.89		-1.58

Sequence ID NO	ORF	GENE	30 min	1h	2h	3h	8h
SEQ ID NO 327	YNL112W	DRP2	2.82				
SEQ ID NO 328	YNL131W	TOM22	-9.70		1.52		
SEQ ID NO 331	YNL134C		1.12		-2.02		
SEQ ID NO 333	YNL143C		2.88		1.62	-2.87	
SEQ ID NO 335	YNL179C		1.78	2.79	-1.87	1.65	
SEQ ID NO 337	YNL338W						
SEQ ID NO 339	YNR002C	FUN34					
SEQ ID NO 708	YOL052C-A	DDR2					-1.87
SEQ ID NO 341	YOL106W			3.51	2.44		
SEQ ID NO 343	YOL109W	ZE01			-3.45		
SEQ ID NO 345	YOL126C	MDH2		1.91	2.17	-3.11	
SEQ ID NO 347	YOL139C	CDC33					
SEQ ID NO 349	YOL150C		17.69				
SEQ ID NO 351	YOL151W	GRE2	9.20				
SEQ ID NO 353	YOR120W	GCV1	1.54	3.40	-1.46		
SEQ ID NO 355	YOR121C				1.63		
SEQ ID NO 357	YOR122C	PFY1	2.81		1.40		
SEQ ID NO 359	YOR131C			2.59	1.54		
SEQ ID NO 361	YOR261C	APN8	1.76	1.07	-1.10		
SEQ ID NO 363	YOR267C		-2.15				-1.21
SEQ ID NO 365	YOR285W		-18.36				
SEQ ID NO 367	YOR286W						-1.86
SEQ ID NO 369	YOR327C	SNC2	2.19	1.92			
SEQ ID NO 371	YOR372C	ND01		-12.93			
SEQ ID NO 373	YOR374W	ALD4	4.02				
SEQ ID NO 375	YOR382W						-2.17
SEQ ID NO 377	YPL037C	EGD1	-5.83		1.22		
SEQ ID NO 379	YPL078C	ATP4	-4.50				
SEQ ID NO 381	YPL079W	RPL21B					-6.18
SEQ ID NO 383	YPL085W	SEC16	2.28	2.74	1.22		
SEQ ID NO 385	YPL089C	RLM1	1.94				
SEQ ID NO 387	YPL180C	NAB3	2.80				
SEQ ID NO 389	YPL201C		-3.57				
SEQ ID NO 391	YPR028W	ATP15	-12.41		2.40		
SEQ ID NO 393	YPR035W	YIP2					
SEQ ID NO 395		GLN1			-2.78		

C. albicans 522 CDS's				S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for synthCaaX gene	wt mubaX gene	codons used in	frequency: per thousand
Ala	GCU	30.7	8686	x	6	21.1	118595
	GCA	15.4	4357		2	16.2	91018
	GCG	2	578		1	6.1	34546
	CGU	5.9	1682		1	6.5	36518
	CGC	0.7	204		1	2.6	14571
Arg	CGA	3.5	989	x	3	3	16957
	CGG	0.8	220		3	1.7	9801
	AGA	23.6	6673		1	21.3	119672
	AGG	2.7	769		2	9.3	52057
	AAC	37.9	10731		1	36	202351
Asn	AAC	18.7	5293	x	2	24.9	140194
Asp	GAU	43.6	12323	x	5	37.8	212658
	GAC	14.7	4152		7	20.4	114451
	UGU	9.7	2757		1	8	44797
	UGC	1.7	493		1	4.7	26357
	CAA	35.2	9964		1	27.5	154529
Gln	CAA	6.9	1948	x	8	12.2	68463
Glu	GAA	49.5	14001	x	3	45.9	257930
	GAG	11.5	3252		10	19.1	107568

TABLE 8 - continued

C. albicans 522 CDS's				S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Gly	GGU	33.5	9492	x	2	23.9	134515
	GGC	4.5	1281		7	9.7	54629
	GGA	13.7	3874		2	10.9	61481
His	GGG	7.7	2182		8	6	33627
	CAU	14	3964			13.7	77260
	CAC	5.8	1642			7.8	43878
Ile	AUU	39.9	11281	x	3	30.2	169795
	AUC	14.2	4005			17.1	96126
	AUA	12.3	3478			17.8	100027
Leu	UUA	1	295	x	2	26.3	148133
	UUG	36.1	10204			27.1	152590
	CUU	9.8	2777			12.2	68479
	CUC	2.5	694			5.4	30218
	CUA	4	1133			13.4	75414
Lys	AAA	48.6	13760	x	2	42.1	236746
	AAG	19.4	5477			30.8	173174
Met	AUG	18.4	5219	x	8	20.9	117410
Phe	UUU	28.6	8100	x	4	26	146355
	UUC	15.9	4486		7	18.2	102389

TABLE 8 - continued

C. albicans 522 CDS's				S. cerevisiae 11645 CDS's			
aa	codons	frequency: per thousand	total number	codon chosen for synthCaBAX gene	codons used in wt muBAX gene	frequency: per thousand	total number
Pro	CCU	13.2	3722	x	1	13.6	76366
	CCC	3.6	1027		5	6.8	38247
	CCA	26.6	7531		1	18.2	102277
	CCG	2.4	686			5.3	29758
Ser	CUG	3.1	875	x	9	10.4	58583
	UCU	23.3	6595		1	23.6	132608
	UCC	10.3	2928		4	14.2	79928
	UCA	24.6	6955		1	18.8	105570
	UCG	6.5	1836			8.6	48186
	AGU	23.6	6673		5	14.2	79649
	AGC	4.5	1269			9.7	54330
Thr	ACU	30.7	8689	x	1	20.2	113634
	ACC	13.9	3928		8	12.6	70777
	ACA	17.4	4928		5	17.7	99759
	ACG	3.6	1019		1	8	44817
Trp	UGG	11	3115	x	6	10.3	58092
Tyr	UAU	24	6782	x	2	18.8	105489
	UAC	11.6	3280			14.7	82483
Val	GUU	33.2	9391	x	1	22	123726
	GUC	10.3	2927		3	11.6	65203
	GUA	8	2265		7	11.8	66100
	GUG	10	2842			10.7	60033

TABLE 9: Regulation of 23 selected "Bax-specific" functions

Cellular role: Amino-acid metabolism				
ORF	Gene	Control	Bax	H2O2 B vs C
YOR302W	YOR302W	11541.92	26808.35	8895.74 2.32
Cellular role: Cell stress				
ORF	Gene	Control	Bax	H2O2 B vs C
YML028W	YML028W	12889.91	2166.45	11327.36 0.17
Cellular role: Chromatin/chromosome structure				
ORF	Gene	Control	Bax	H2O2 B vs C
YBR009C	YBR009C	2149.69	8655.43	2909.14 4.03
YDR224C	YDR224C	13661.40	55858.34	18829.27 4.07
YNL030W	YNL030W	8676.99	19603.93	4732.39 2.28
Cellular role: Energy generation				
ORF	Gene	Control	Bax	H2O2 B vs C
YBL059W	YBL059W	2728.21	8786.71	1644.48 3.22
YGR183C	YGR183C	23181.54	81865.40	24053.00 3.53
YJL166W	YJL166W	5296.71	18093.93	5001.65 3.42
YLR038C	YLR038C	7338.65	19935.69	5118.43 2.72
Cellular role: Signal transduction				
ORF	Gene	Control	Bax	H2O2 B vs C
YHR135C	YHR135C	3939.64	8358.11	3707.17 2.12
YOL100W	YOL100W	2218.45	6088.96	2619.31 2.74
Cellular role: Transcription factor				
ORF	Gene	Control	Bax	H2O2 B vs C
YDR216W	YDR216W	5925.91	18459.00	6434.43 3.11
Cellular role: Unknown				
ORF	Gene	Control	Bax	H2O2 B vs C
YDR504C	YDR504C	2741.47	6908.49	2839.62 2.52
YGR146C	YGR146C	2099.74	5616.94	1303.89 2.68
YGR236C	YGR236C	17717.80	64439.96	24134.29 3.64
YHR138C	YHR138C	6218.30	14817.41	5220.50 2.38
YJL142C	YJL142C	6988.27	16006.02	8740.46 2.29
YKL123W	YKL123W	2826.82	5952.34	2766.04 2.11
YLR414C	YLR414C	4510.80	11867.69	3531.27 2.63
YMR107W	YMR107W	13453.15	78850.98	17417.00 5.86
YOL099C	YOL099C	3690.45	11604.72	5454.15 3.14
YPL201C	YPL201C	15960.14	33633.74	7449.66 2.11
YJL060W	YJL060W	8798.50	2406.39	6356.11 0.27

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CLAIMS

1. An isolated nucleic acid representing a synthetic BAX-gene selected from the group consisting of:
 - a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences, or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
 - a) providing (a) genetically modified yeast or fungi according to claim 11,
 - b) treating said genetically modified yeast or fungi with a mutagen,
 - c) isolating resistant yeast or fungal cells, and,
 - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
 - a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
 - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
 - c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
 - a) providing a genetically modified organism according to claim 10,
 - b) expressing a cDNA library in said genetically modified organism, and,
 - c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732.

d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and

f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),

20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.

22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.

23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.

24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.

26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.

5 27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.

28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.

29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 32.

30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.

10 31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a polypeptide having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

(d) a functional fragment of any of said polypeptides as defined in a) to c).

15 32. A polypeptide according to claim 31 for use as a medicament.

33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.

34. An antibody according to claim 33 for use as a medicament.

35. A pharmaceutical composition comprising an antibody of claim 33 or 34.

20 36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOS 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOS 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOS 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and

(g) the complement of any of the nucleic acid molecule as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

10 39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in a pharmaceutically acceptable carrier.

40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus.

15 41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- 25 (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- 5 (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- 10 (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- 15 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in frame with a reporter gene,
- 20 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- 25 (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- 30 (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.
49. A compound or polypeptide according to claim 48 for use as a medicament.
50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.
51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.
52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.
53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.
54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.
55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.
56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenous flora of humans and other mammals.
57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.
59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.
60. A compound identifiable according to the method of claim 59.
61. A compound according to claim 60 for use as a medicament.
62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.
63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.
64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.
66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.
67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

69. A pharmaceutical composition for use as a medicament for treating proliferative disorders of
5 for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as
defined in claim 36 or a human homologue thereof or an antisense molecule to at least one
of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian
homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human
homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient
therefor.

70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.

71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

72. An expression vector comprising a nucleic acid as defined in claim 20 36.

73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.

74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.

75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.

76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.

77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.

78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.

79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002W, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGAATAGTAGTAGTCATGTTGTAACTCTCGCCCTAAGTATACGTAACGAAATGGTA
GCATCTCGGTTATGGGCCCCAGGTTAATGTGTTGAAATTCGCATCACCTTTGAGA
AATATGGGAACCATCTACGCTGAGCTTGGCCACCGTTCCGCTAAATAAACGGGTGT
CTCAAATTTCTCCCGGTTTTCAGGATCAGAGCGGCATCTAGTCTGTGTTAAATCGGCG
TTACAGAAACAAGAAAGAAACATCGCGTATATGCAACAGTAGACACATTCGCCGTCATAT
ATAAGTTTTCGATCAGTAAACCGTATATTTGAGCATTAACACAGGTTTAAATATATATTT
ATAATCATGTGATATGTAATAATTTTTCGTGACTGTTTGTGTTTATTTATTTAGCT
TTTTTAAAAATTTTACCTTCTCTGTGTTAAATTTTTCCTGATGCTCTATCTCAAAACCAAC
AACAACTTACTCTACAACTAAATGTCCTCTCCGCGCAAGAAAGAACAGACTCTCAAAAGCTC
CAGTGAAAAGAGACGCTGCTCAAGAAACAATCAACTCCGTCGTGATGTTGAAGAAGAT
CTAAGTTTAAAGAGAGAGACTATCTCTCTATATTTACAAAGTATTTGAAGCAAACTCACC
CAGACATGTGTTATTTCCAGAAAGCTATAGTCTATATTTTGAAGTCTCTTTGTTAACGATATCT
TTGAAGAATATGCTACTGAAGCTCTTAAATTTGGCCGCTTATACAAAGAATACTCACTATTTT
CTGTGATGAGAAATCAAAACGCGCTTAGATGATCTTACCTGGTGAATTTGGCTTAAACATG
CCGTTCTCGAAGGATCTAGGCTGTTTACCAAACATCTCTCTCTCTCTCAAGACCTTAA

YBL002W, 131 aa (SEQ ID NO 22)

MS5AAEKPKSPAKPAEKPAAKTSTSDVQKKRSKVRKETYSSYVYKVLQJOTHPDPTGLSQ
KSMSTLNSFVNDIFERIEATEASKLAAYNKKSTISAREIQTVRLILPGELAKHAVSECTR
AVTKYSSSTQIA

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAATATATGGGCAATATTTGACACTTCTCCGGTTTCCCTCCCGCGCTCTCGTATCCGCTCGCATTTTGACCTCGAGCAAGCGCTCCACTATGTCGTATATATGTTTACAGTATAAACTTCTTAACGTGTGATATTTTGAATCTTTAACTCAACCCACATTCAGTATACGGTGCATGATATAGAATATATCTGTATAGCATATGTTTATCTTTCAATATATGCAAAAGGTCGACCCAGGACAGACCGCGGTATTTTCTATCATATCCGTGAATATAGGACACCAAGTCGGCGGCTATTTTTTTTTTTTGGCAATTTTTTTCGGGATGGTTCCCGGCAAAAGCTAGACCCCGGAGATTTTAAATATACGTATAAGAAACAAGAGCCGGATGTGCTGCTATTTGTGATATATAAAGAGAAGGAGAGATAGAAAATTTGTGCTCTAGATCTTCGGCAGTAGGATGAGATAAATTTTCAAGAAGACAGGAGACAAAGAGATTTGTAGTAGAAATTTGTAGCGCTCAATATAGAGAGACGGCATGGACCCTTCTTAGCAGGCTCACTTCGATACACAGAGATTAAACATTTGGCCACAGCACCTATCTGTGCAAAACAATTAACAAGATGATCAACCAAGCATAGGAATAAATCTGTATGCTCTTATTTGATGCTGTGACAAACGGTTGGTAAATTCAAATTTTTAGCATCTTGGCGCATCTTTGGGGGTGTTTCTCTCACCCAGCATTTCCCGCTGTACCAACACCGAAGTCAGGCCCATTCGCCAAATTTGAAGCCGGAAATTCGACAAAGAAATTTGTAATTTGATCGGCTTTTCAGTCGAAGATGTGTAGTCCCACGAAAATTTGATTTCAAGACATCAAGGAAATAGCAATAGTTTAAATATTTGGTTTCCCAATTTTGGTGACATCTTTAGAAACGTGGCATCCCTTAATATGATATGTTAGTCGGAAGGATTTCAAATATCATGATGGGTCTCATGAAGACCGTGAGGCTCTGTTTCTGTCATCGATCCCAGAGAAAGATATAGACTGATTTTACCTACCCCTTCCACCGTCGGAAGAAACACTTCTGTAAGTCTTAAGGTTAATCGACGCCCTTGCAATTGACTGTACAAGAGGGGGTAGTAATCTCAATTTAATTTGGCAGCCAGCTGACGATGTCAATATTCCTCTCTTGTCTCCCAATGATAGGCGAAGGCTTAAATTTTGGTCAATTTTATGAAATTTAAACCTTATTTAAGAATTCACCAAGTCGAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MF8ICSQAQLKRTAWTLPKQAHLSQSTIWTATAPILCKQFKSQDQRLRNRNSDAPNFDFA
D7TVGKINFYDYGDSWGVLFPSHPADFPUCTTEVSFAKAKLPKFDXRNVKLIGLSVEEDV
ESHEKWIQDIKEIAKXKNGVGPPIIGDTFRNVAFLYDMVDAEGFKNINDGSLUKTVTSVFI
DPKKKIRLIFTYPSVTVGRNTSEVLRVLDALQLTDKEGVTPIINQWPAADDVIIPPSVSND
AKKQGFQFNEIKPYLRFTKSK

4/251

YBR289W, 905 aa (SEO ID NO 64)

MNVQPGOTWSVPSNIGNIFSNIGTPSFNMAQIQOOLYQSLTPQOLQMTQQRHQQLLRSLRSL
 QOOOQOOOQOTSPPTQTHSQPPPPQSQPTANQSATSTPPPPAPPHNLHPQIQGVPLAPA
 PINLPQIQIQLPLATQOQVLRQQAIAKNNPOVNAITVAQOOVQRQIQEQKQSQQTAAQ
 TQLEQQRQLLVQOOOQOOLRNQIQORQOOQOQRHHVQIQOOOQOQOQOQOQOQOQOQOQO
 QOOOQO
 LPKLANPKYQIQYDQPETKLPYTYWSDKKADTDULLYEQIQORDKINKSLYLRBTWGY
 DFFSYIGVQYKIESRHMHTLKYYQDULNTMRKSIYSTQKPSASWGNQSGVGNGIT
 NTFYVFIPOVEVGNRKHYLEDKLVYQOQAMNETSEQULPVRLEPQDQDRDFRLDRLAWN
 KNDULKIEDFVDDMLRDYRVEDATREHQHITQISTEQIQEQGNPVIELNDQORLGD
 DLIRIKLIDVWGQONIQDFEWIINSNDNCPEEFASBMCQELPGEFVTAIAHSIREQ
 VHHYKKSALLGYNFGDGAIEDDDIIRMLPTTLDYVRAAEASKFTPLNLLQIQISAEL
 ERLDKDQDRTRRQRSGNRGMLALSGTASNTSNVGHVTVAAAGNSALLPPEGLL
 PDIAIDPRTFRTPVPSLPMGVDGVSVESYELRNTTYTKVNTVAAGNSIRAGVTIPISIP
 PGHSULLSTYKLGKVNNTKEEPAAPNDTSGTWAMLPSPESLKTKLNSNIRAGVTIPISIP
 NPIANHTVTNSRNPLOQVPIPGGAASKSVPTPSLPIAPPVAPHDSEATLJTNNSNGSSNN
 NTONT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

[illegible]

YCR004C, 247 aa (SEO ID NO 70)

MVKIAIIITVTVGHIDVLAQVKKGVEAAGKADIYVEETLPDEVLTQMNAPQKPEDIP
VATEKTLLEYDAFLFCVPTRFNGLPQWSAFMDKTGLWAKGSLNGKAAGTFTVSTSSVGG
QGESTVRACLSYLAHHGIIFLPGLYKNSFAELASIEVHGSGPWGAGTLAGPDGSRITASP
LELRIAETQGTFTFYETAAKLFPKAKEAKPSTEKKTTTSDAAKRQTPAAAATAEKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

TGAAAAATGATCAAGGCACATTCTTTAATTGAAGNAGAGAGAGAAACAAAAATTAA
ACCGATTGGACCAATATATGCTCTGAATCGACAGGATGAGAAATATTTCGAGAGCAATTAG
ACTTTTCTTTTTCGAAGTGGGATGCTGCGACGACGAGAAATACATCTACTTGCATCTA
AAGATACAAATAGATGGTAAGAAATTTGGCGCGGCAAAAGGCTTCAAGCTTACACAA
ACGGTTTATTTTGGAAATATCTCTTCTGAAGCTTTTACGACGACGAGAAATTTTCGATCT
TATTTAAACTTTAAATACGCTGAACCGACATAGAAATTTGAAATGGGAAAAAAAATCG
CATTAAGGCATATAAAGAGGCGCAATTTTTTTTATATATATATATATATATATATATTA

5/251

AGATAAATAATAGTCTATATATACGTATATAAATAAATAATTTCAAATAATAATAATAATAA
CTATTATTATTAGCGTAAGAGGATGGGCAAGAGAAAGAAAAAATTTGATCTATCGATTTC
TAATCAATTTCAATTTATTTCCTTTCGGATAGAGAACACACCTGGCAATTCCTTACCTT
CCAATAATTCGAAGACGACACACACACACAGACATGGGAGATCTTGTTCAGTGACAC
CGTACTCTTACGACAGAGTGGCAGGTGCACACACCAATTCAGCGTGTTCACGACG
CAGAGCTCTTCACAACTTGTCTATAAAGCCCTTAGTACAGCAGCGGAATCTTTCGAAAT
CGAAAAACACTGTGTGGACCGTTTCAGACAAATGCTCTTAGCCTTTTCGACACAGTAGGACGA
CTCAATTTCTAGATCTTCGGTCCATTTGTCACACCTTTGCCAGCAGCTGGAATACCTCTCT
TGTCAGTGCACATCTTGGTGTGGCATCAGCAGAGAAAGCATCGACGAATGATGAAGTCTG
CTGGCAAGACGACTTCGACACCCCTTGTGGCCCTTGGCCCTTTTCATCAACTTGGGAAGATTA
CAGCAAGAACCGCTGTGCAAGATGGAGTACCAGATTTCAGTGTCTTTTCCAAAAACCTTCTTGA
AGGTGAAGAAGCCATACCACCAACCAATGATGATGAGTCGACCTTGTTCACAACAAGTTGTCA
TCAATTGA

YCR013C, 215 aa (SEO ID NO 78)

MGKEKRKLIVRFNSIYFSDKKATGCSLPSNNSKCAPPVETWEILSVTPYFLATV
AVSPPMWTVLPAAEILUTSSNKALVPAANFNSKTPGGFQTMWLAFAVAANNFLDSG
PLSNPCQAPGISVTVVLVASAKSAMKSTGTNTTPIALASISNGTISAPALSK
MESPISVFSTFKVKAIPPPMMIESTISNKLISIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTTCGCTAAATTTTACTTTGGAGACAGAAAGTAAATTTTGTTCCTCTTC
ATGGAATAAGTTTCCAAAAAGTCTTTAGTAATTAACCATATGTTCTTGTATCTGGCGCTGC
GAAGAAAGGTTAGCGCCGCGCATACCCATATTTGTATTAATPAGCAATAAGAAACAAT
TGTGAAGTTTCTTTTAAAGTATATAGTATTCGATATTCGATTTTCACTTGTATAAAT
TGGGTATTTTATTGACCAATATATCCGCTTGGACACTAAATGCTTTTCAAGTTGGTGCTAC
GTCACTGCTTTTTCAAATGATCTGGGGCAATTCGATTAGAGGAAGCCACAGTTTGGCAAGG
GCAGATATGATAGGAAGACGATTAACGCAAGGAAGGATAAGAAACATATTTAGGGAGTCTG
TCGACATTTAGACCATATGCTTTTGGACATTAAGAGGTTACGAGGAGGAAGACATATTT
CAGGATTAACAGACAAAAATATAGCATATTAACGGTTACGAGGACCATATCGTATG
ATTCGACTACATACGGCACAGCCGGGCTTGGATATAAAGATTTCCAAATCATCTGAAG
ATTGGAATTTGAAGACTTCCACGCGCTTGTGCGTGAGAGGATTTGGGCTTCTACAGTCCA
AGATGGAAGGTAACACGTCAATATTTTACCATAATTAATAATTTGGGAAGCACACTTAT
CTAAGCTGATACACAGGGCATGCTCTATTCAGTTTCGTATGAATAAATCTTCGGGTATGATG
GTTTGGCGAATTTGATGTTATAGATTTGAGCGCCGGAGTGCCAGCCCTTCACCGCGATGAA
ATAATTGGAGAAAACACCAACATAGTAGGTTCAAGTATACATTTGTGTCAGAAAGCCCAAG
TAAAGTCTCCTTAAAGGATGGCACACACAGATGTTGGTGCGGCTAGTAGAATTTACTT
TGCTCTCGAGAGGTGAATTTATACAGGTGCAAAAAGAGGCTGTAGCCGATTCGGTTAA
AGAAGGCGTTATTTAGCGTTTGAATAAATCATCTCGATTATGACATTAAGATTTACAATA
ATACTATCTCGATGGCTTGTGCTCAAAAAAATTTAAAAATGAAGCTAACACCAATTT
ACAATTTATGTCAGGCACTAATAGCAAGCCGACCTTTTATCAATTTGGAGGATTCGTTAAG
GCACGCATATCAAAATA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSSTSYSDTTVGTAPGLDIKEFQIITEDMNGRPASAMSVQRIGLLQSKIERVY
NIYNNKYGKNLSKLIPEHALIQPANETFGYDGMWDVIDVEARECQPTFVAVNGENTN
TSEVKYTVAAEQVKVTLKDGNTTQCGGLRITLSRGECYNRKSKEAVGDALKALLSF
EKIILDVETKLTNNYVVDGLYGSKKIKNEANTNYNLLSNKPTFIKLDGAKGTHIK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTTCTCTGATTTCAGCAATGGCCCTTTTCTTTCTTCTCAGATCATACTCTTCCGCTT
GCTTTTGGAAATCTTTTATTTCTTACTTTTGACGTTTGTTGACCTTGAGTGCACCGG
CCTTCAAGCGCCCTTTAAATCTTTAACTTTGAGAACGGCAGCTGATTTGATCTCCCTT
TTATTTGCTTCTCAACTGCTACTTTTACAGTAAATTAATGAGCAACCTTCAGATGCTTCT
CGCTAAATGCTCATCTGAATATCAATTAATTTCTCAATAAATCTTAAATTTCTTAC
TCGTTCTGTACGGCTCATCGCCCAATATTATCCCGCTTGTATGTGATCTTTTGTGATCTT

8/251

TGTCGAGTACTTTCGAGAACCCAAAGAAATATATTCCTCGGTATCCAAAGATGGCGTTTGGCGG
GGTTGAAGAGGAAAGGACAGAAACGATTTAATTACTTATATGACAAAGCGCTGCACAAAT
AG

YEL039C, 113 aa (SEQ ID NO 142)

MAKESGTFKPGSAKGAATLTKFKTCQOCHTTEEGPKNVGNLHGIFGRHSQGVKGYSTTD
ANINQNVKWEDESMSEYVLTNPKKVIPTGNMAFAGLKKKEKRDNDLITYMTKAAK

YER112W, 1064 bp, CDS: 501-1064 (SEQ ID NO 147)

TACTGAAGTCCCTTAAACCTACTGCTCTTTTATTTTAGGCTCTAAATAAACCATGACGACA
ACGTGAATGGGTAGCATCTTTTATTAATAGATAGTTTATTAATGATTAACAAATATTTA
AAGATATTTCATAGATAGTAAATTTTAAATAGTTTTAAAGTACTACTTTTCTTTTACCG
CCAGTTTCTCTGATGATGAAAAGGCAAAATCCGCATTTGTAGCCGCCACACGCAATTTTG
ATCATTAATTACGAATTTGCCGACAGTGTACGTTGATTAAGCACTCTTACTATCATGT
TTTACGGATAGCAATGATGTTCAATTTATTTGCACTTTTCTTCTGGAATCGTAGTATCA
TAGACCTTCTTAATGATGAAGCGGTAAAGAGGAATCGTGAAGATTAATTAACGAAGT
AGTATTAGTAAACAGAGTTGAACAACTGATAATCTTCAACTCGAAGTGAAGAAAGAAACA
CAATAGATATTTTCTCAATGCTACTTTATATCTTTTAACTGCAAGTGGAGGAGCAAC
AAATGCAATAGAAATGAAGAAACGGTGAATATATACAAAGGATATTGACCAAGCTAGATA
ACTGGATGAACCTTACTTTATCTTAATCTAACCGAATATAGTGAAGAAAGCGCAATTAAT
CAGAAGAACTGTAGACAGTGAAGCCGTAAATTTGAACCAATTTATATTAGAGGA
CTTTTATCAAGTTTATCAAAATCTCAAGATATAATTTGACAGAGTCAAGCAGCAAAATTA
ACTCCAACAACTCTTAATAGTAACGCCCTGGGCATTAAGAAAGTAAACAATATAGG
ATTCAACAAACAATAGAGGTAACTACAAACAGAACAAATAATTAACGCGCAACGCAACC
GCCGTCCATCTCTAAACCGCTCAATTAACAACAGCAAGCAGCAGTAACTAATTAACA
GTATCAACAGATAGCAACAGCAACCAAAATATGAACAATGGTTTAGTGGTCCGCTCC
AACATCATTTTAAACAGCTCTCTTCCACAAAGGTCGAATTTAA

>YER112W, 187 aa (SEQ ID NO 148)

MLPLYLLTNAGQQQWQIELKNGELIQGILTNVDNMWMLTLSNVTEYSBESAINSEDAES
SKAYKLEIYTRGTFTKFTKLQDNIIDKVKQIINNNNSNSNGPHKRYNNRDSNNRNG
NYNRNNNNGNSNRPRYSQNRQYNNSSNINSINSINNNQNMVNLGGSVQHHFNS
SPQKVEF

>YFR010W, 2000 bp, CDS: 501-2000 (SEQ ID NO 153)

GAAAAATTTCAACGGTGTCTCTAAATGGTTTCCCATGATATCTCTGTTATTTGACTCTGT
TTGTAAAGAGATTTTGGGTTTTCAGAGCAAGTACTGTCAAGAGGTTTCGAAGTACAAATTTA
CGACTATAGAGATTACATCTTGCGAGTCTGCTGATGCTGCGAGTGTGGTTTAAAGCATTTG
ATTATTTAGGAAGCACTCAGAAATATATTTTCCATAGAAGCCTTAAATTAAGTATGCAATTC
ATAGCCCCATGATACCTTTTCTTCTGACTACTTGTATTTGGAATCTTAATTTGACCTAACTGG
GCATCTCGGTGATTTGTTATATATGATACATTTTACGTAAATAAGTACTGGCTTAATATAA
AACATAAAATCTACAAAGAGGGTGAAGTGTCTTTTGAATTTTGGCCACTGCAAGTAAATTTGG
TGCATTTGAAATACAGATTTTCTGTTCTTCTAAGAGGATATAAAATTAAGGAAATTAGCCCT
ACCTATCTCTGTTTAAATATACGAGCGGAGAAAGTTTGGTGTCAATATAGCAATTTCTG
GTAAAGTTTACCCCAATACATCTTTCCACTGATGCTCTCAGCAGATTTGAAGGTTGCTGT
CTGGGAAAGTGCCTAAATAATATATCCCTTAAATCAAGCCAGGATCGCAGTAATGCTAT
TGGGACTTCCAGATGCTAACCTGATTTCTAAACAGGCCAAAGAAATTAATTTCAATTGAAG
ACCTTGGCCCTGAGCAACAAAGTCCAACTTTGCTCAATTTGCCCTTTGGTTTTCAGAAATA
TGGGCAACACCTGTTATCTGAATCTACCTTACCTACAGGCTTTATACAGAGTGAACGATTTAA
GGGATATGTTCTTATTAACCTTCTCAAGGTGTCTTAAACAGTGGTGCACAGATG
AAGAGATTCCACAAACAAATCGTTTATTAATGAATGAAGCGTTGTTTGAATAATTACAGAAATA
AAATTTGCTCAAGAGTGTGGCCAAATGTGTTTATTAACACACCTGAAGAAAGTGTATCCAC
AAATTTGCTCAAGTGTATCACAAGTGGTCTTATTAACACCAAGCAGCTGGAGGAGTTGT
TTACACAACTATTCATAGATAGTATGTTTGTGTTGTCAGAAATTTTCCGAGGATTTCA
GGATTCATTTAAACTACCATCAAGACACAGCTAATGATGATACGATATTACTGTTAAAG

9/251

AAAATGAAGACGGATTTCTAAATTAACAATGTCATATTTCTGGTACTACAAATTTTCATGAGAA
ATGGGCTCTCTGGAAGGTTTGAATGAGAAAAATGAAAAAAGATACAGACTTGATGGCGCCA
ATTCCATCTATACGCTGGAAGAAAGAAATATCAAGATTACCAAAGTTTAACTGTTCAGT
ACGTTAGATTTTCTCGAAAAAGGTCACCAACAAAAATCTAAAAATATTTGCGGTAAAGCTCG
TTTTCCCATTTCAATTTAGATGTTGCGAGCATGCTTACCCAGAAATACGCGACAGAGAAGG
TAAAAAGTCGTGAGCAACTGAGAAAAAGTTGAAAAAGGAGAAAAATGAAAGGAAAGAGAGA
TCAAAAGGCGTAAATTTGACCATCATCTCCAGTGAATAATGTCATGACACCAAGAGAACAAAT
ATGAGACACACAGTGGCTCTTAAACGAAAGTGAAGAAAGATCAATGGCTCGAAGAGTATAAGA
ACATTTTCTCTCAAACTGGAAAAAGGTGAAACCCCATCTTTGTGTTTATTAATCTGATCGG
GTGTCATTACACATCAAGGTGCCAATTTCTGAGTCTGGACACTTCAAGCTTTTCTATAGGG
ACGAATCGACGAAATAAATGTPACAAATTTAATGATGATAAAGTTAGCGTTTGTGTAAGAA
AGGAAAAAATTTGAATCTTTAGCCGTGGGCGAAGAGTAGTACGCTGATCTTAAATGT
ATAAAGGATTTGGTCTGTATA

>YFR010W, 499 aa (SEQ ID NO 154)

MSGTEFENIRHSGKYVPIITLSTDATSADLKSABELTQVPSARQKVMYKGGLSGBESIK
IYPLIKPGVTVMLLGTPDANLISPKAKNNPIEDLAPQQVQFQALPVGKNNMNTCYL
NATLQALYRVNDLRMLNPNVPSQVSNAGQDEBIHKQIVIEKRCFENLQNKSPKSVL
PIVLNLTURKCPQPAERDSQGGFYKQDDAEELFTQLFHSMSIVFGDKFSEDPRIQFKTT
IKDTANDNDITVKENESDSKLQCHISCTTTFMRNGLLEBNEKIEKRSDLTGANSIYSVE
KKISLKPFLTIVQYFWMKRSNKKSLIRKVVFPFQLDVADMLTPEYAAAEKVKVRDEL
RKVEKNEKEBEIRKRPDPSSSENVMTPREQVETQVALNESEKQDMLVEYKHKHPNPL
EKGENPSCVNLIGVITHOGANSESHYQAFIRDELDENKWKYFNDDKVSVVEKEKIESL
AGGESDSALILMYKGFGL

>YFR052W, 1325 bp, CDS: 501-1325 (SEQ ID NO 157)

CAGAGACATGTTTAAATCAAGTATGAGCGGGAACGTCGAAGATCTCTAAATGAAGGAT
AAAAAGAGTTCTTAAAGAGGAATAGGAATAACAGAGTAGAAAAACCGAAAAAGACAAC
TTAAACAATCGCAACACTTTTATGCGGCCCTCGCTCGCTGTGCAAGTAGTATTGTTGAC
CTGGAACAGCATACACAGAGACAGCAATAGTCCGTACAACTAATATTAGTTTCTG
ACAATGCTCGCTTTTAAAGCCATGCTAGTCCCAATCAAAACACTTTTACTTGGCCCTGAA
GTCTCTTTTTCGTAGCTGTAACTTAAATAAGCCATCTAACCTTTTCTTTTCTTAAAT
TTCTTTATTTACCTCTCGCTTTATTTCTATTCTACACATTTATTTGCCACCAATGAAA
TTGTAGCTTGTATTAATAGGAAAGCGGAAGTATAACCGGTGGAAGTACTATTGGAAG
TGAGATAAGACCATGTAATGCCCTCTGTAGCCGAATTTGACCAAGTCTGTTAAGCATAG
CCTTTGAAAAACGGGATTAATGCGCGGTGAGAGAGCTTTGCCCCCTATCAAGATCGAAC
TTATCAAGATAACCTTTTAAATACCTGACTTATCTCATTTCAAAATGACATCTATTGAAATG
ATTTGACAGCTTTCGGAATTTACTTCAACCAATTTGAAGCCTTTACTTCTAGCATCCAACTTCA
ATAAATTATCTGAATCTGACAGAAATCGAAGCTGATAAGTCTGTATTGTTGAACTTAT
TGCTCAGATAACACACCACTTCTACTCGGAATTTGCAAGTATCTAGATAAACCATATCA
AGAACTTGAACAGCATTTCACTTTTGTCTTACCCATCAAACTAGACAGATGCTCATGG
AAGGTCTGACAGAAAGCATGGGATTTCTGCAATTTGGGTGCGCAGAAATATATCAAGAT
TCGACTCTTTTACCGATATCTTAAATACAGTATAGAGAGCAAAATGCTTAAATAATACCG
AGCTACTACGATCTTCTCTCTCTCCAACTAAAGGCTTTGCTCTTTTCTTCAACACG
AAAAAGAACTCAAAATTTGCACTAGAGAGAACTGSCCTATTCTCAACTCGAAGTTT
ACTTCAATAACCAATCAAGGAGAAAGCTGATTACGAAGATAAATGATGATGATGAAGAG
ACCAAAAGACAAACATTTATCGAAAAAGCAATGGATTATGCCCATAGATTGTAATAATTG
TGATA

>YFR052W, 274 aa (SEQ ID NO 158)

MPSLAELTKSLSIAPENGDYAAECKLLPPIKIELIKNLLIPDLISQNDIYLNLDLMTKR
ILEVGAALSIQTFNDFSFNYPNQLKPYFSSNNHKLSESDKSKLSLSLYLLSQNNNTT
KFHSELQYLDKHTIKLEDEDSLSYPKILDRWLMBSGSYQKAWDLLQSGSQNISEPDFSTDI
LKSARDEIAKNTLSYDFLPLNSIKALLFPNNEKETEFALERNNWPVNSKVYFNNQSK
EKADYDEDEMMHEEDQKNTIEKAMDVAISIENIV

12/251

>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2: 880-1244 (SEQ ID NO 169)

TATATAAATAATCTTTGATAGACATATAAATAAGAAATGCCCCATTTTGTAACTTACCGGAAA
GATGCCAGTACATCCCTTTTACACCCGTCATTAAGAGTGTGGTGTATTAATAGAGCT
TTATCATATCTCTTTGATTTCTGCTGCTCGGCTTGGGACTCACAGAGATCT
GGAAATTTTCATAGTTGTCAGTCTTAGGATGGTTCAGTAGAGCGTGGCCGCGTGA
TGGAAATTTCCAGATTTTACACATAGTGTGGAAATTAATAGTAGCAATAGCTATC
TGGCTACTGTTTTTAAAGTATTAGCCGCTTCTCAGTCTCTTTTAAAGGATTAACAAG
GCAAGCAAAAGATATATAATATGCTTGAAGCAATCTCTAGGTATCTTTGGAGGATAG
ATAACAGTAAAGATAGTGAATTTCCGTCACGAAATGTTAAACATAAATGCA
AGAGAACAATTAATGAATGATTAATATTTGTAATAAATGTTATGATAGGAGGA
ATGTACCTAAGCCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATTCAATTCAGGCTTAGGCTTATAGCACTCAACGATTTTAAAGCTTTGTGTATTGC
TGACATAATTCAGGCTTAGGCTTATAGCACTCAACGATTTTAAAGCTTTGTGTATTGC
AAGAAATAGGAGTACGTTTATATATTTGTAATAAATGTAATGATATCTCCGTTGATGTG
GGCAACATAGATTTAAGTGGATGAATAATTAATGCTCATTTGTGAAATAAATAAATTTG
CTTTTACTAACAATTTTATTTATTTGTTTCAATAGACGTTTCTCTGACAGAA
AGCCAGAAAGGCTTATTTCACTGCTCCATCTCTGAAAGCTGTGTTTGTATTGCTC
CATTTCAAGGAATTGAGAGCTCAATATGTTATCAAGGCTTTGCCAATCAGACAGAGC
ATGAAGTCTTGGTGTGCTGCTGCTCAAGAGGCTCAAGAGGTAAGATTTCACTGTTT
ACAGATTGAAGTTTGTCTGCTCAAGTTGACAGGCTCACCAAGGAAAGGTCACCGGTGCT
CCGTTCCAATTTAAGTCAAGCTTCAAGCTTGTATCAATAGATTACACTTGGACAAG
ACAGAAGGCTTTGATCCAAAGAAAGGCTGTAATTTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTWYSSDRRKARKAFATAPSSERVLLSAPLSKELRAQYGIKALPIRRDDEVLV
VRGSKKGQEKISSYRLKFAVQVDKVTKEKNGASVPINLHPISKLVITKLHLDKRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

TTTCGAATATTTTGTGAAACAGGCTCGAAAGTATCTCTTGTCTAGAAATATTCGGT
TGGCGGTGGTGTCCATATCTTGGTGTCTGTACTACGGCGGTACTACTGTATTGGTAT
TTTCGGCATTTTCCACCGACTAAACATCCCTTTTGAAGAAACCAATAAGTTGTCCC
ATAAGCATTCGAAATCTTACGCTTTTCTTAACTAGACTTGGCAAACTCTGCTATCTT
TCTTATATCGCCCACTTCAAAATCTCAATTTGAATCTCTTACCAATCTCTGCTGAGGAA
TTTTTCTTCACTACATCTATTTTCACTGAAATCACTAAGTTTCTGATTAAGGTATAG
ACGACAGTTCCAAACGGTGACCTTGGATCAAAATATATGCTTGTAGCGGAGTTTATTC
TAATATCAAAATAACTTATTTCTCTCTTCTTCTTCTGCTGCTGATGCGCCACCGCTGTAG
ATAGCGAACTAAGTGAAACATGTCTTCTGCTTACCTATCTCGCGGAGAGCTGTACAA
GATATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
GAAATGTAAGACGAGTGAAGTATTCAGGATATTAATTATACATACATACAAAGCAAG
ACAAAGAAACATTTTATAGATTAACATTTTACTTCAATTTTGTGTTTCTTCTTCTTCTTCTT
AGAAAGACCTGCTGTGTTAATGTTGGAGTAATCCGCTCCCTACTCTGATCTTCAATAA

>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYPLLPSTYHPNHLFPSPISIFFFFFFRNCLPRIVKDEV
KYSGVYVYIHTKQDKETFLDLTFYFNCFCIPYKNDLLLFNVGVIRPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTATAGATCTACATTTTACTTCAATTTGTTTGTATTTCTTATATAAGA
AAGACCTGCTGTTTAAATGTTGGAGTAATCCGCTCCCTACTGATCTTCAATAAATGTC
TCTGTATCTTAAAGGAGCGCTCCAGTACTCAATTAAGCACCACCTAGTGGCTGTAGTGT
CGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
CAATGTGATCTACAACTATACAGAAAGTAAACGACCTATCTATCTTCTTCTTCTTCTTCTT
ACGGCAATATTTAGACATATCATAGGGGCCCCAAGGGAGAAATCGTTAAATTTTAAACTTTT

13/251

CTTTGCTCTTGAATGAATAAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
TTGAATTTTAAAGCAAAATTTTGTGATTTAGTATGATATAAATAAATAAATAAATAAATAA
GGTAAAGATTTGGTTAGTATGAATAGTAATGAACCTGGATCTAAGAAATAAATAAATAA
ATGAGATTTTGGTTAGAAAGAAATCAGATCTTCAACCCCTACTCAGTTGTTCTCCG
GCTCCAAAGTTCAGACAAATCAATGAATTTCTATCACTAACGATGAGGATGAAGATA
CTCTGAAGTAAATAAAGGCTTCAATGAAGATATATACACTAGGGGACGACACCGGTG
CACGCTTAGGATAGCAGGCTGTTCTCCCAACCAATTAAGGCAATCTCCTGCTGCTAC
ATATTTCAACAAACCTTAATTAATCAAGTCCAAATCTTCAAGGCGATCAGATTTTCACTTA
CCATATCACTACATTTTCAAAAGATATGAAATGTTTGTCTCTCACGTAAAGGTAACAGTTG
CATCTCTTCACTATTTATCTTTTCCAAAGAGTGGCAGTCAATATGGGGATCCAAACC
AGCTATTAACGCTCAACTCCAAAGAGTGGAGTCAACGATGGAGTTTACACAGTTCAT
TCAATGGAATAATAGTTCTTCTAGCACCTCTCTTTTATTTTGTGATTTAGAGTCTACGAAA
CCCAAAATAGAGCTCATCAAACTCTTCCAAATCAATCTAGTCAATATCGACCCCATACTA
ATCAACACAGCTCATCAATCAAGGTCCTCAATCAAGTCTCTCTCTGACGGAAATAT
CCATGATAAGGCGCTTGTGTTTATCTGCTACCTTTTATCTACTAATAGCAATTAAT
TCAACAGACCATCAATTTGACCGCATAAAGATGGGTTACTTTACAGAGATTTCTT
TACAGGAAACAAGCAATTTGATTTATCTTTATGTTGATCATAGGAAAGCTTAGATGTAAT
TGGCATGTTGATCGGAAATCTCTGGAAGCTCAAAATTTGTTCCATCAGCTACTTTATG
ACCATGGCTAAGAGATTTCTGATCTGGAGATTTACGAGTTATCTTTCAGAACTCAATTTTA
TGGCACATCTGCTGAGAGTTCTACTTCAATTTGCCAACACATTTTCTTCACTCTCTCTT
CAGTTAATCTCTGCTACTTAAACTGAAATATATGTTGTTTGTCTCCATTTGACACAT
GTTATCTCTCTACATGCTCTGGAATAAATTTGTTGCTACTCTATTTCTTCTGCCCCATTT
TGCACCAACAGGCTTAAATTTTACATTTAAATTTAGTGGTGGTCTTAAAGAGAAATATTTCT
TAGCACCTGATAGGAGGATGATGAACGAATTTCTTGGACAAATTTCTGTACCAAGAGGG
TATGGGAATCATATCCAAACCAACAAATCAAGAGGAGGAGGCAATATATGAGTTGTTTA
CTACAGAAAGAAAGTTGTAAATCTTTGGAATCATCCGAGATCTTTTCATGAAGAAAT
TATTAGAAACGAATATTTATTCATCTGATGAAGATTAATTTTGAAGCAGCTTTTCTG
CACATATCAATGAATAATATCTGTCAATAGAAATTTTGAAGGCTTTTAGCACAAAGGC
AATCATTTAAGCCCAATTTGCTCTGGAATTTGAGATATATTTTGTGCGATATCTCTCTTCT
TTGATCTCTTTCTGTCTACATACATAGCATCAAGCATACGCAAGATATCTTAATTTGAACCC
AAAGATCAGTTAATCCCAATTTTGTCTGTTTGTGAGATGAAGTGTCTAATTTCTTCCCTGA
GGCATGGATCGATTTCTTCTTCT
TGTAAGAGATTAATACATCTTCTGGAACCTAGTAACAGACAAAGATGATCTCAAAATG
TAATGAAGTCCAAAGATCTTTTAAAGGCTTATGAAAGGATTTCTATTTCAAAATTTGAAT
CAGCACAGATCTGTATGACGTTAAGTGTAAAGCAGAAATTTCTATTTCAAAATTTGAAT
ACCTTAATCTGGTGTGAAATACGAAATAAGGAAATTCAGCATGAAAGGTTTACTCTCAA
GGAAGGAGTGAACAAACAGATGCTCTTTTACAGGAGACATTTCAATTTTACCTACTCG
ACATATGCTTATTTCTTGAATCAAAAGCTGTAAACAGTGGCACCACCAACACACTGTAT
TTCAGAGACCAATTTCT
TAAAGAGATGTGACAGAAACCAAAATTTGCTCTACGGGCTGTCTCTTACCCCAATATC
AAAGGCAATTTCCAGAGATGCTATTTGATTTGCTCTTATCTGCTTACGGTACGAAACCAATATC
AAGTACTTTTGTGCGCGCGGCGCGCGGATTTACAGACATTTAATAGAAAGGTGAAC
AAGACAAATAAGGCTCTTGTGATGAACATAACATATTTACTTTTAAAGCAATGGTAGGTC
AATCTTTCTACTCATACATAAATCTAATCTGCGCTCAACGATGCTCTTAATCTGCTGCTG
GTAAATTTTATTTGGTGTGCAACAAATATGGGACTCTTTGTCTTAAATTTATGCTATGCTAC
TCAATCAAAACAGCTGCTCTTCTGACACAAATAATCAATTTTACAGATCTCTGTATTTGG
AAGATATAAAGTTATGATTTCTTAAATTTGACAAATAAGTGTAGCGCTCTCTTTTAGAGC
TAAATCGAGATGACAGAAATGACAGATTTTCTTTTCAGAAAAAATTTCTAAAGTGTATTTTA
ATCATGTTTGAATTTTCAAGAGCGGTTCCTGTAATGTTTAAAGAAATCATTTATGATTTGCAC
ATCATGTTTGCACCGCGCACAAATTTTATGATGTTTAAATCTCTTGTATTTTATTTTAA
GGGTAAATTTTAAATAAATCTTAAAGGCGGCTTGGTAGATTTTGGGCTGTGATTTCTGTAAC
CTCTGCTCTTTTCTTTTGGAGAAATAGATCTGCAATTTGCTTGTAAATAAATAATATCAAAA
TATTAAGCTACCGGAAGTGTGTGATATAAATTTGATTTTAAATTTAGGGAGCTTTTAAATCT
TACATGATATAAGATTTTAGGAAACATGATATAAAGAGAGCTTCAAGTAGTGTCTTCCATCT
TTCCGATAAATAAATTTTCAACTTTTGTGATTTTCTTCCAGAACCTCTGCTTCTCAATAAGC

AAGGAGAMAGGAGGAGACAAAGGATGTTTCTATTTGGAGGGGGAACAGAACAGTTCG
14/251
CGATGCTTACCCCTATATATTTGGCAATTAATGTAACTTTATTGAAATTTGACATATAG
AAATGTGGAACATTTGGCCCTGTGACTTGGAAACAAGATGCGATGTGAATCAATCATTAAG
CCAAAGAGCTTATATTTGTATTTAGAGATCTCTCAAGATTTGAAATATTCGAACGTGTAA
ATTTTGA

>YGR070W, 1155 aa (SEQ ID NO 174)

[illegible]

1364 bp. CDS: 501-1364 (SEQ ID NO 177)

>YgH3132(.1356 bp, CDS: 301-1000)
 CATCAATGTCATACGACGATGAGCTCTCGATGATTCCTCAGAAATCCAGAAAGTTGGCATATT
 ATGTATATAAGCGGATGATTATGTATATTTTATGTGTCTCCAGTAAGTCGACAGCATATAC
 CGGCCAGTCGTGCGTCAACAGCTGTGAAGCAGATATATGCGATATATCAACATATATTC
 GCTTCCGTCAGAGATTGTGAAAGAAAGAACTCTAGTAAGTATGATTCACATACATCTTGG
 AGCTTTTACACCTATGCCAATTAAGTTATATCAAGTATAGAGATCCACATGATGAGATTA
 ACTGCTCTTCATGATGATGATCGGGTTACGGGAATGTTTCCATCAATATTTTCAGGAA
 GGGAGTTTGACAGTCTCANGATGACACGGTTGAGGATATATATATTAAGCAAAAGAA
 AGAAAAAAATTAATTCGGTAAACAACCATCAACGATACGGTACGAACTTAACTCAAAATG
 ATAAATTCTTTAGAAATAAATGCTCAATCTTCSCAAACTTACAGATGTCATCCAAAG
 TGCATTCGCCCAATGGTGAATATTTGACAGGAGATTCAGAGGATTCAGTACTCCANGTATGATGTAAG
 GTGGTTCTGTGTGTATATTTTCGACAGATCATGTGTATGAAACAGTGTGTGGGTG
 AAGCAACTATTTCTTGGTGCCCTTGGCTGACAGAAAGCGCATATATACAGTGTAGAGCA
 AAGCAATGACATTTGCTACCAATACGTGTACGAAGATTTGCAATGTGTCTCATTTGACT
 TGAGAGTCTTACCTATACACAGAGTCTTTACAGTCTACCCGCAATATACCAAAATTTGGGTC
 TCGATTATACAGCAAAAGGTTCACATTCCTGGCAATGAGTCTTTTAAGCTCTATATAGT
 CTCATATTTATGCTGCTGCTTATATCTCAGAGAAATTTATTTCTCAAAAATTCAGAA
 CAAAGCTTTTATACGAGGCCAACAAGATTCGGTATTAAGTTGGAAGATGTCATATCACTC
 ATATGACGTTTGTGCTCCGAATTCACGAAGCATTTGACAGCAAGCAATTCACAGCAAG
 ATGCCGAAAGGCCAAATTTCTTGTGCAAAAAGCAGAGCAAGACCAAGCTTCTGTTA
 TCGAGCTCGAAGTGAAGCAAGAAAGTGTGCAATTCATTTCAAAGCTTACTAGCTGATG
 GTGATGCTCTGTTATTTGATTAAGAAATTGAAAGCTCTATAGCAATGCTCTCAACATTAG
 CAAACATCATCATGCTGTCTATATTACCAATCAACATTTCTGTGTGTGTAAACAGCGAGT
 CTTCGGGATCCACAAATTTCTGCTTTTGAACATTTGGCGTTAA

>YGB132C. 287 aa (SEQ ID NO 178)

SYGRISZC, 2018. 02. 22. 14:00:00
MSNSAKLIDVITKVALPIGIIASGIQYSMTDVKSGSRGVI¹FD²RINGVKQQWEGETHFLV
PWLQKAIITYDVRTKPKSIATNTGTKLQWMSILTLRVLHREVLQLPALYQNLGLDYDERV

WO 02/064766

15/251

1277 bp. CDS: 501-1277 (SEQ ID NO 179)

[illegible]

YCP135W 258 aa (SEQ ID NO 180)

YGR3135W,258 aa (1569 LP NO 2507)
 MGRSRDSTTTTFSSEGRRLQYVEALELSSHAGTACIGMSDGIIVLAERKVTLSLLEOD
 TSTERYLYRNDKNAVAVALGTJDAELLINAPRIHAQVLYLKYNDIIPVILVIRLSLDIQK
 GYTGHGGLAPFQVSTFYAGSDYRQYLYLTNSPBGNTGWKLSIGVANTSAQOTLMDQY
 KDMKAVDDALTELAKTLYTSSALLTYLTLRFATIRKGNAGGEVYQKIFKPQELKILIV
 KTGITRKDEDEADEDDMK

WCD155W 2024 bn. CDS: 501-2024 (SEQ ID NO 181)

[illegible]

18/251

TTTATTCACATTAACGTGCTTATACGTGACCTCTTAATTCCTTCACCAATCTTTGCGT
GCACCCGTCACAGAAAGCGTAGAAGAAATCGTAGCTACAAAATTTTTCAGATTAATA
AGTGCATATGTTTTCATTAATGTCACGCTACATCAATTAATATTCATCTGTTCTTG
CCAAAATATACAAAATGCCACATTTTTCCTTACACGGAAGAAATTTGGCCGTCGCG
GACAGCGCTCAATTAATGCGGCTAGATTCCTACGCTGGAAGAGTCAACCTGTATG
AAACATTAATGAAATCTCCAGGTTTAATACATAGAAGTTTCAGGCTCACTAATAAA
AATACCTTGTCTGTTAGCTAGATTAATGTATCAATTAAGTAAACAAACATGATAT
TCGGGATTTCTCCCTAACATGTCTTATGACGTCCGCAATTAATCAACCTACACTGAT
AACGTGATGAACTTTCTGCTCTCTCTGTCAGTCAACCTCACCACACTGATCAT
TTATGAACACATACCTGCTGCTGTAAGCATTAACAAGCAACCAAGGCTTTAAACCTT
TTTCTACGTGTCATGATATAATTCATGCTGTTGGAAGATGCAATGCACTGCTACAAA
TCTTCAAGATTCAGGGTTACCAAGAGTTCCACAAGTCTTCTACAGTACAGATGAAT
TGATGAAAAATCAAGACGTACACGCTATCGTAATGAATCAAAACATAGATGACGT
AAAAAATATACAGATCCCAAGGATCTAGTTTGTATGTTGTTTTCATTTCCGCAATTC
ATCAAGTAGACCTAAATATGCGCTAGTAAGGATGCTGTTTTCATTTCCGCAATTC
CCAATTAAGATCCGTACAGAAATTTGTAATGTAAGATCAATGAATTAAGTCCGCTAGCAAT
TAGGTAGATGATCCATGATGACATGACATGACATGATGAATTAAGTCCGCTAGCAAT
GGGAATGAAGGAAAACTCTCCGGAATTAATGGGATGATGACATGTTGCTGCAATTTAT
GAGTCTTGCGAAGCTATGCGCTGACATGCTGTAATCTATGATTAATGCTGACAAATTTG
CCTTAGGTACCTGCGACAGAAATTTTCATTAAGATGAATGATTAATGCTGCTCCCAATTCG
TAACATACATGATACACAGTACTCCAGAACTGAATAATTTATGCTGCTCCCAATTCG
CTGCTATGAAGAGCGGGCTTATGTAATTAATGCTCAAGAGGTGCTTGTAGATTTTATTC
CATCTGAACACGCTAAGCGCTCAAGGCCAACAAATTCGAGGTGCTGCTTGTAGATTTTATTC
CAGTGAATGACGTAAAGAGTTCAATTAATTAATGATGACATTAATGATGACGTGACATTC
CTGATGTTGTTTATTAACAAATTAATATCTGACACCAATTAATGATGACATTAATGATG
AAGCTCAAGTTCAATGCTGATTTGAGTGGCTACTGATGCTGATTTGCAATTAATGATGATG
GTACTGCTGCTGTTGTTGAATCTCCAGAACTGATTTGAGTCTTGGACATTAATGATGATG
AAGAAACACAGTACGCTGCTGATTAATTAATGATGATGATGATGATGATGATGATGATG
TTAATGATTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG
TCGCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AAAAATGAACCAACTTCTGCCAAATTTCCATGACATTAATTAATTAATTAATTAATTAAT

>Y1074C, 469 aa (SEQ ID NO 220)

MSYSADNIDJDSFORAMNFGSVPFAMSTPSQSFMTLPRRVSTTKPKALKPSTGDMN
ILLENVATTAIKIPFDQGVGFPHKSLPEDELEIKIDVHAIGISKRLTEKILDHA
RNLVCIIGFCIGTNDYDLRYASKGLAVENSPNSRSVAELVIGELISLARQEDRSIE
LHTGMWVAAACWEVRKTLGIIGVHIGSLSVLAEMGLAHVLYDVIIVIMAGTARQ
VSTDELINRSDPVLAVPATPETEKLSAPQPAAMDGAIVINASRGTVDVIDPILQAV
KANKTAGAALDYVPHRPAKNGESFNDELNSMTSELVSNILPHLPGSGSTEEAQSISG
IEVATLAKVINEGNSVGVNPEVLSKSLDYDQENTVRVLYIHANVGVULKTVNDILSD
HNIEKQFSDSHEIAVILMDISSVNSEIKDIEKLNQTSKVSIRLLY

>Y1R037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCACATCTTTTGGCGGATTTCTTCACCAACGCTTCCATTGGAACCTGTCGTA
TGTCCAGACAGATAGACAAATTTGCTGACAGTATCTCTTCCTCAAGACTGACAC
TACCTTCGCTTCTGTCAGCGCTGACAGATGATCATGCTGCTTCCAGAAAGTGT
TGACCAATTGACAGCAATCCACGGGAGCACTGTATCAAAATTAACCTTGCCTATAT
TCACCAATTGACAGATTAATGATTTCTCTGTTGCTGCTGCGGAGCCCTTATTTTC
CCCTCTTTGACAGATTAATGATTTCTCTGTTGCTGCTGCGGAGCCCTTATTTTC
CTGTAATTCCTCTCTCTCTCTGATTAATGATTTTTCAGTCTTCCATTAATAAGGTCAAA
AAGTGAAAAAAAGAGGAAAAACATGAGAACAGTATGCTCCCTTAATAAAAAAGTCAAA
CAATAGTATTAATAAGACATCAGAGCTTTCACGCTCTCTCTTCAAGCTGTCAATCTC
GTAAGTATTAATCAAGTTATATCATGCAAGATTTCTATAGCTAGACCTGTTGACAAAG
GCCAACATCCCTTCGACCAATTAAGGAAAAAGTGTGCTTATGCTTTATGTTGCTC
GCAAAATGTGATTAATCTCTCAATTAATAAGAACTAGAGGCTTGAACGTTAATAGG
ACGAAGGATTAATCATGATCGGTTCCATGCAACCAAGTTTGCCACCAAGAACTGAGCT
CTGATGAAGAAATTTGCCAGTTTCGCCAATGAATAGCGGTGACATTTCCCATTAATGA

19/251

AAAAAATGACGTTAATGCTGACGACATGAGAACCTGTTTACAGTTTGTGAAGCCAA
AATCCGATATGTTGGCTTGAGAGTATCAAAATGGAATTTGAAAAATTTCTATGATGA
AAAGGGTAAAGGTACGAAAGATATCTTCACTACCAACCACTTCTGCTTGTCCGAAA
CCATCGAAGAACCTTTGAAAAGAGGTGAATAG

>Y1R037W, 163 aa (SEQ ID NO 222)

MSSEYKLAIPVDKRGQPPFDLKGKRVLLIVNVASKGFTTPQYKELEALYKRYKDEFTII
GFPCNDPGHGPESDEHIAQFCQJNLYGVTPPIMKKIDVNGNEDPVYKFLKSGKSEGL
RGIKMNEFEPLVDKRGKRYERYSSLTFRPSLSSETIEELKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATTAAGTCTGGGGGCTATTCCTGCACAAATTTTCATATGCTTCCATATGTAATACCTG
TTAGTCGGTATCCACAGGTGAACCTGTTCTTATCAATAGAAACATATGAGTCTTCTG
ATATGCTTAATCTTGCCTCATTAATTTTAAAAATTTCTTCAATGATTAATAGTTATTC
TTGAGCAGATGATGATGATATTTTATTAAGAACATTAACCTGCTAATATATATGATCA
GCTTAATAATTAAGAAATGCAATCAACAAAGTTGATTTTCTGCTTCCGATTCGATTCGAGT
CCACATTCAGACCTCTGCTGATGATGATTTGCTGCTTCTGCTTCCGATTCGATTCGAGT
TAATAACCTCCGATTTTATTAATGATGATGATGATGATGATGATGATGATGATGATGAT
ATTAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATGAGATGCTTTCATATCATATATGATGATGATGATGATGATGATGATGATGATGAT
CCAGTTTTCAGGACATGCGCCAAATCTTGGCTCAAAAGTCTTATTAATTTGCAAGGATTA
TGTAACATGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATCAATATGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACATTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATCAAGAGAAAGGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT
GTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTAATAGCAATTCACCTTAAGGAAATAATCAATCTTTTAAAGGAGATGCTGTTAGTG
TTTAGGCTTCCACCGGTGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT
AAGCTGAGTGGCTTGAATTA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLRHNSQTFKFSSTSPNLGSKPLFSKGNLYSLVLTLYGTGLACLYLESINLAK
SKEDPHALIAEDDIIVADIPNRIFFKPAIDYOEKELDLQKSLDHLVHLSTYSVDSQ
FSIWMFLLIQLSSLLIGNSTLGRKSLIYKGSVSVLGRPPLIYMAKLKLRMKLEKGVME

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GTAATTTCAAGAAATGACACACACAAAGCCAAAGCCATTAAAGTATGATGAACAATG
GGACTACAAATGAAATTAAGAAAAATAGAAATAGGCTAGAAATCAATTTATTAATGCG
CCTATCTCTCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAAACCAAAACCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTTTTGTCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTGATATGAGGAGGAGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
AGCATTAAGCAATGATTTTACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TTCCAAAGATGCTTTTGGAAACCTAAGATTAATTAATTAATTAATTAATTAATTAATTAAT
ATGAAGTGTCAAGTGGGCTTACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AGAAATGTTGGCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AGAAATTTCTTCTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
CTGCCATTCGGCAATGTTTGAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT
TTCAATTCGCCATGGAAGTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
CGGTTGATGAAGATTTGGTAAAGTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
ATGAACCTTTGAATCTGGCAGAACTGAAGACACAGCAGTGTCAACAAATGAGATTAAT
CACTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AAGCTTTGCCCAATTTGTGTCAGGCTACAAATTAATTAATTAATTAATTAATTAATTAATTAAT
GCAAAAGGTGAGACCGTAATCCAGTCAAGTTTGAATTAATTAATTAATTAATTAATTAATTAAT

20/251

ATTTACCACTACCGAAGACTAAACCTGTGGAAGGTTAGAAAGGTAACTTCGACGCCTACA
ACTTTGAACCTGTCAGACGAACAGATGAATAATCTTGATCATCCCTGATGCTTATGAGCCTA
CCGATTTGGGAATGCACAGACGGCCCAATA

>YJR096W, 282 aa (SEO ID NO 234)

MVPHFKYLSNGFKIPSIALGTYDIPRSQPAEIVYEGVKCYRHFDTA/VLYGNEKEVGDGI
 IKWLNEDPGNHKREEIFYTTKLWNSQNGYKRAKAAIRQCLNEVYSGLOYDILLIHSPLBG
 SKRLTEWRANQGEAVDGLGKCYGNYGNYGKIKDELINDELPHKHPVNVQTEISPMWNRQ
 ELADYCKSKGLVWEAPVGLCHGYKYNTPDGLKVCKEVDNRNGQV/LINWSLQHGLYPLPKT
 KTVARKLEENLAAYNFELSDEOMKFLDHPDAYSPTDWECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGGCTAGGTTTCACATATACAAAGAAGTTATGGCTTATGTGCTCTTCTTCAAGTTTGA
CATTTATGCAAAAAATTTCTCGTAGATCCGCCCGTGAAGCAGAGAAATATTTTAAAGT
CGGCATAAAAAACCTTAGAATAAGAAAGGAGAGAAACATAAAGCAGAACACCACTACT
TTTAAAGGCTGACGAAACATGTGTGGCTTATCATATTTGTACTTACTTACTTTCGCAAG
TCCTTTTACCCTCTCGATAGCTACTGCTTATGCCCTGCACAATTTACATGTAAACCCGACG
TGCATGCTATATACAGAGATAGTTAAACATAAAGGCGGGCTACTAAACCTCTGGGCGCA
GTGCAAAAATAGAAATATATGCCAATGCGGACTTGTATAGTTTCTGCTTTAAAGCTATG
GTGTCATTTGCAACGCTCTCTTCTGCTATCTTTGCGAAAGTGGCAAGTCTTAAAGCAATTA
GAAGAAATAAATAATATTCGGAAGATTTATATCTTACGACATTTATTTTATGCTCACATG
TTGAGGTGGTAAATAGCTCTTCACTTCTGTTTGGCTTTGGCTATCCGAGTCGGTAGGGGTA
TTGTTTACGACCTTATATACCAATTTGACAGGAAGCAGCAATAAAAACTATATATTTATAA
CGGGTTGTCTTGTTGGCTGTGTTTATGATTCATGSAAGAAAGGTCTCAAATTCGTGTGTT
CATTTATACCAACAGCAACAGCTGCTCAATCGGGTCACTCGCTGTAACTTCCCAATACAGG
CTTAGCATCAAGAGCTGTACATCAAGAAATATGTATATTTCCGGGTGTATCATTTGTACT
TTCTTCTGTATGTATCCCACTGTCAATGTCTTATTTGTCGAAGAGACTGTGAAATACCAAGGCT
TAATCAACGAACACAGAAAGCAAAAAATTGAACAAACCTTCTCTCAACAGCAGCAAGAAAGACT
CAAAATGAAGCTGATTTCCACAAACTTCAAGAGGAACATAAGGAAAAAGCAAAATTTCTCTGG
AGGGCCTTACAAAGCAAGTCAAAAAAATCTCTGGAGAAATATTTTGTATGAGAGAAATCAACCTG
GAAATGTAGCAGCTGCTGAAGCTTCCAAAGAGAAACCTTAA

>YKL065C, 206 aa (SEQ ID NO 242)

NSLSYFTTLFLLLTVEVMFLFVLPPLPRIRGRISTYVQLTAKQIKTIFITGCLVLG
LFTDSWKRSQIRVSLXHNDSIGSSAVTPQALASRAYVNOVMYISGFLVFSICPT
VMSIVRLVKYQGLINEQGEQKLRPNSSNKSDSNEADSTKLEERKKQISLEGLQKQV
KNLEKYFDEKNNOVAAREASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

[illegible]

21/251

ACAAATCGGAGTCATTAAACGGCAAGTTCCTCCAAAATGTTTATAGCAAGCTAAATAATCCA
ATTCTGTTGTCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRYYIGVFRSGGEKALELSEVKDLSQGFPPSSVQGPWTFPAETVASRTGAGQROJSIE
EGNYIGHYVABSEGTGVLITDKEYVPVPAYTLNKLILDEYLVAHPEEWADVTFETNDAL
KMKQLDVTYISKYQDPSQADAIMKVQQLDETXYLVLHKTITENVLQGEKLDNLVDKSESIT
ASSKMFYKQAKKNSCCITIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEO ID NO 259)

TAAATAGTTGAGGCTTTTCTCGCATCTCTGCAAGAAGAGGTAATGTGATGAACAATGCAAAAT
GACACTGTAAAAATGATTCATTAATCCCTGATATGAGAGTGAATTTCTATCTCTTTTCTTTT
ACATTTAGTTTTCATTTATATGCAAAATAGAGGGTATACAGTTGAGAGTATTTAAACAATTGA
ATATAAAAGTGTACAGAGGAACAACGAGAAAGGCTTGTGTGACGCAAACTTCTTCATCA
TTTATTTTCACTCTTCAGAGGTCCTAGACCTTTTGAAGTATCAATATAGTTTATATCA
TATCTCTCTGTCTTCTCGTTACTATAGATATATAGTCAGCTTCTGAAATTTACACGCC
TATTTATTTGTTCTAGGCTCAACCCCTCTCAACCCTTTCTTGTATATAAAGGTT
GTTAATTTAGTTAAGCTCTCTCTTACCTACTATCAATGCTTACGAGAAATTTTACCCAAACC
CTCGCAAGATAAATAGAAATGTGCAAAACAGTGGCGAGTGGTACAAACAGGAGCTTTTCA
AAAGACAGGTTTCTGCTTCTCAGAGAAACAATCTTAAGCAACAACCAATATATTAAGCGAG
AAAAGGGAAGATATTTGTTTATGTTTCACTTGCATGCCATGGGCCATATGAACAACATAA
TTACAGGGCTTTGAAGGGATTAACCTCTGTTATAGATATAGCTAGTCTCAATTTGGCACC
TTGACAGAAAGGATGGAATTTTGTGGACATCGAAAAGCAATTTGGAGGACAGTGAAGATT
TTTGTGGAACAATTTGCGACAGATGTTCTAGTGGTATTAGAACTCTCAATGAAGAGTATTCACGA
ATAGGCTTTGCGCGACGATCAAGAATGACACTGACTTATATTTACAGAGCGATCTCAATCTCG
CTCACTATGGANATCAAGAAATCAAGTGAATCTATATTTACAGAGCGATCTCAATCTCTCG
CAAGTTTCAACCGTCCAGTCTGTGGAGTATTAGAACCACCAACAATTTGTTTAAACAACGAA
GTAGCGAAATTTATTAAGGATTTTGAACCTCTAGTGGCTTCGATGAATTTTGTGACGAGCAT
CAAGAANAACGGACTTTGTTCCCTGCTGTCTTGAACAACAGATCGATGATCTTCAATCTTCT
GGGTTTACGACAGCATCACAATGGTGTATACAGACCGGATTTCCGACAGAAAGACGAGAG
TTTACGAAAGTGAAGTCAACAACCTATTTGAACAATTTGCAACAAGTGGAGAAAAATCTCTGA
GTGCAAAATTTCTCAATTTGAAGCCAAATACGGTGAAGAGATAGACAATAAAATCTTCG
GTGAGTTTCTTCCATCTGGGTGTCAATTTAACAGAAAGCTGACATTAAGTATCTATCTAGAG
TCATAGATTTCTGATCTGTGTACGTCCAACTTTCAATTTGCAATTTTACTCTTATTAGAG
CGGATATCAATTTATCTTGTGGTATGAAGAAATTTATCTGGAATATGATGACCTTCA
GGTATCAACAACAGATTTTGGCCATATGATGACCACTCAACGGCTTCCCAACAAGATCA
ACCCCTTTGGGAATTTACGCCCTGGACCCCAAGACAGATTTCTGCTCTTTATTA

>YKR076W, 370 aa (SEO ID NO 260)

MSKQWASGTXGAFKQVSSPRTSKQHPYYPKGRVWLVYSLACPWAHRTLITRALKG
LTSVIGCSVVHMLDEKWPFLDMEKQLDSEDFLEHWHVDVAGGTRTAKEDSSKSPAEIK
NDSQREWADTNEPHGYKGLSDLYSKDQSPQYPTVUWDLTEYTNVNNSEIIR
LNNSSAFDEFVDDHGHYGLVQAKTQIDFNSWYTSINNGYVGTGAEKAEVYSEVN
NVWFELHDKVEKILSDSKYLKAKYGEEDRQKILGEFFTVGQDLTEADILYTVTVIRDPV
YVQVHKCNFTSIRAGYFV IHLWNRNLWNVYDAFRYTFDFDHIKLHYTSHTINPLGITP
LGPKPDIRPL

>YKR092C, 1721 bp. CDS: 501-1721 (SEQ ID NO 261)

CCAGAGGATACCTGGTGAATCTACGTCGTCTCTACCTTTGGTTATATACCTTTGCCCTC
CTTTTTCACCTCTGGTGTGGCGGTGTTCGAGCTAATAAGTTCCTTTATCGCGAGAGGGGTCT
ACATAATCTGTGTTTTCTACCTCAATTAAGCGACTATAGCAATTTGTATTTATACGAA
ACGATGTTCTGTCGCTTCTCGATCTCTGTTTCTGTTTGTAGTCTGCATCTCTTTATGT
CTGGATCAAAACGATAATTCGACCTATTGCAATTTAGTTCTCTTACCCATTTCTTTATC
ATAACGGCCGAGAAAAAGTGAAGTGTTCGAGGAAGCTTTGCAACGGGAGAGGAAAAAC
CTTTCCATCGCTCAGCATACATTTTTTTTTTTTATCAATGCAGGCTGAAAAAAAAT
CCTTTGATGATGGAATCTTCGACTTTTATCAAGCAAGAACCCAAAGTCGCGAG

24/251

AGGTAAACAAGCCTTTTCAATATCTTGACAAATTTGGAAATCTTCTGGACAAGAAGTACA
CAGATTTTGGAGCGGAGTATGTTAAGACAACAAGGACAAGATACTAGATCGTACTATTG
CCATCGGAGACATCTGACCGAGGCGAGCTGAGACTCTATCCCAACGATGATAAGTTGG
ACGTGGTATACCATCAACACTTCAATGCAATCTGGCCACCATCAGAGATGATTATTCCC
GTATACACATCGCTTCAAGAAATATATCTGCGGCCAAGAGCTTCCAGCGCAACAGG
ACTTTACCCACATAAATCGCGATATCTCGCTCGCAGCCACGGGTCAACCCGATTGGGA
TCACCCCACTGGGCCCAAGCTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)

MSEKSAENKAEFRKQSPFRELISDHPIYKPAKGRWLYVALPCPWAQRILITRALKG
LAPITGCSVAHWHLDDKGRFLDEEGDKNERHWFDIAGGISVNLANTSTPVANPNNAH
RLLVGDDEPHVGYKRLSDFYFKTKPDYKGRFTVPVLWDLCTCIUNNESSDIIIGMNSA
AFDEFVGEYRQVRLVPSLELAQITFNSWVYDKINNGVYKAFGAECVAEYEREVTSLFQ
YLDKLENLDDKYITDLEAEYKGNKKILDRYFAIGDTLFEADVRLYPTIVRPDVVYHQH
FKNLATIRDDYSRIHTWLKNIYWRHEAFQRUTDFTHIKLYTRSQRVNPFIGITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATGTGTCCTCAATCTGGAATAAGTCTACTTCGCACTGCTGCTGCTGGATTAATATCC
CTGAAGGATACCTTCAAACTCTGTAGGAACTCTCTGGTTATAGATAACCTTTTAGCCT
TTTTTACGTACTTATACCTTTAAATTTCTCTATGTATGATATACATTAAGTTTCTACT
TATGTGNAATCTTATCGACCGACCGGCTTTTGTACGGAAGTGAATAAATCTAGCTT
TGGTTTGTGTAAGAATATTTGGAGACATATAAGTACCTATATCTTGTATACGGAAT
CAATAACAAGTGTCTGCTAGTGTATTTGAAGTTGTCAGATCTAAGAGTAGAGAGAAG
GTGCATCTAATAGTGTTCGACGTTCTCTCTTTTAAAGTTTATTTTGTGCTCTCTAGA
ATTTAAGTCTTAGTATAGTTTGTGTTTGTGTTTGTGGTTCATATTTTCAATTCAGAGA
GAAATTTAGCTCTTTTATTAATTTCAATAGAGATAACGAGAGATGCTCGGTACTACAT
CAAGCGATAAGCGGATCGCTAGTCAAGGGATAACCGAAGTCTGAAGTTTGTATGCTG
CAGACTCTTGTACATAAGAAATCCGACGCTATAAAACCTAAAAAGATTTGTCGATGGGT
CAATGGATTCTTATTTAGTCAGATATAGATATAAATTTCTGCTGGGAATCTAGTGGT
GAGCATATGCTTGCAGACACATCACTGCTGCTCAATGCGCAATGCGAACAACACCG
TTAATAACACAGATATAGGATCCAACTCGCTAGAGAACTTGCATGGGAGGTTAACT
CAGGATAGAAATCTTCAATAGACATAACAGAGTAACTTCTAGGTATATAAAGAGTTG
TTCAGTCTCCATCAGGAATTTAAATGCTACGTTATTAAGAAACCTTATTTATGGTTT
CCGCCAATCAACACCTTAAGTTAAGCTGATATTTCTTAGAGCTTGTACAGATACTTT
TACAAATATACAACTAAGGACATGGTGAAGATAATGATGGGAATGCAATGAATAA
ACGATATTGAGGATTAATGGGAGGATAAAGAACTACAATCATATGAATAAAGGAGAACA
ACACTATCACTTGAACAGGGGCTGTCAAGGCATGGAAACCGCTCACTAATACGAGGC
GAGACAGTCCCTTCAACAGTAAATAAAGTCGAAGAAGATCTCCAAATAAAGAAGA
GACGAGTGTCTTTAAGAGATATAAATCAAGAACTGACAAAGATCTCAATAGTGCAGGAC
TAACCGACAATGATGCCATTAATAGGACCACTCTTAGTATGGCTGGTTTCATATTAC
ATAAAGAATGATCAACACACCGAAGGCAATATGATGAAGGAGATATGGTTTTCATA
CTTCAACAGCGATACTTTGGATGATGGTGAATTTGCTCCAAATATGCCCAATCAATAA
CCATGACATGGCTGAACAGCTGCTACATGAAGAGGAGTAGATTCAACACTTATCGAATCA
GGTCAACAGAGCAAGAAAGAAGTAGAACAAGTGTGGATGAATGAATAACGACGACG
AAGAACGCTTAAAATTTGACCAAGAATCAATAAAGTTCGAATAGATCCGCAAAATCCC
CTTTTAGACGCAAGTAGGATTTCTGAGATATAGTTTCCCTGGGTCAATTTGGTGATT
TTCAAGAATTTATTAATCATTAACAGACAGTCTAGTGGCGAGTGGGAACAAGAATGGGA
TAGAATAAGAGCCGAGAGGTCACCGTCAAGGTTTCGAATGACACACTAGAACAAAGT
TAAGATTTAAGAGAGGGAACAACAGATAGTTTAAAGCCAGCGCAACGATGACAAACAG
AAACGAAGGACATCTGTCGAGAAACCGATGGACATGGTTGAAACATTAATATGACGAG
AAGACGATTAACGAGAAACCAAGGGGAGATGAATAATGAAGAATCTGGATTTCACAA
GAATGGCTCGACATTTCCAAATAACATTTATTTCTCTATTTAATGCGGTGAGAAGA
CGAGGTGTCTAAATGAAGAATAAGCAATTCGAAGTACTTCCACGCGACATCAACAGA
CAAGACAGAAATCGAGAAAACTTTTTCGGAACCTTATTCAGAGAAGGACCAACCAAGC

25/251

ATGATGCAATCATCATCACCCTCTGCTGCATCAGTCTACCATCAATACCAAAATAACG
ATGCGCTGCAGCTTCCGCTGAGGAAAGCAAAAGCTTTGGTAACAAGAGTGAAGGAGC
CGTTGAAACCCATTTGTTGGCAATCGCCTCTGCTCTCACCGTCACCATCACAGCCGTC
ATGTTTCCCAAAAAATAAGGCTAAAAACCTTTAAAGATTTCTCAGCCGCGACGACAGATAC
CATTAACAACCAATTTGGAAGGCGCAATAGAGATGAAGAAAGAGAGGAAAGGATTCCG
AGCTTGTGCCCAACTACAGCCGCGCTTAGTGAAGTAGTACCAAAAGTAAGTCTTAGAG
ACAGAGAAGAGAGGAGGCAAGAAAAAGAAACAAGAGAGAGGACAAATACGACAGAAATTT
CCAACCAACAACACTCCAACACGTTCCAAAGGAGAAATACCGATGAGCAAAAAGCTCAAC
TACAAGTCCAGCTCAAGAACAAAGTCCAAGTTCAGTCCCAGTTCAGCTTCAGCCCCAG
TCCAAAATTCAGCCCCAGTCCAACCTTCAGCCCGAGTTGAAGCTTCAGCTCAAACTCAGG
CTCCAGCGCACACCATTTGAACATACCTCCATATTTGCCCCCAAGAAAGCTTACATTTG
CAGACGTCAAAAAACCTGACAAACCAACTCCCGGTTCAATTCACACAGACAGTGCCTTTG
GGTCCCACCTGCTTGTCTACAGTGTCTAGCGTTATCATGTTCGACCCACCGCTTACCAA
TTAAGCTCAAAAGGGCCATATACCGCTAGTCACTTGAATTTGAGCAATTCGAAGAGGG
GACTCGCGAGCAGGTTATTACTAAGTAACTCATGTATGCTTATCTGAAATCTGGTTAATG
ACACTCTGTACATGAGGAGGTAGCCCAACGACAAAGAACAACAACAACAACAACAAC
AACCCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRNESMLRTTSSDKAIASQRDKRKSEVLIAAQLDNEIRSVKNLKRISIGSMDLID
PELDTKFGESGSRWSGTTSSASMPDPTTVNNTRYSDPTPLENLHGRNGSGLESSN
KTKQNYLGIKGVHSPSRKLANVLKNLLWPNQHPNVKPNDFLELVQDTLQNLQS
DNGEDNGNSNENDIDNGEDKESYENKENTINLRGLSRHGNASLIRPSTLRRS
YTEFDNEDDDNKGDASSETVNVKVEERISIKERPVSLRDIETELTKISNSAGLTNDIAI
TLARTLSWAGTSDDKXQPOPEGHYDEGDTGFSTQANTLDDGEFASNNPNNNTWMPER
SSLRSSRTYAIRSQEQEKEVEQSDVMENDDEERLKLTKNTIKVEIDPHKSPFRQDE
DSENNSSPGSISGDFQDIYHNRQSSGEWEQIEKEAEVYKVRNNDTVQDLELRREGT
TDMVKPSATDDNKETKRHRERNGTWLNKMSREDDNEENQGDDEENVDVSQRMELDNS
KKHYISLNFNGTEYENKEMNSSTSTATSTQTRKIEKTFANLFRPRPHKHRSQSSSP
SSSPSSPSIPNNDAVHVVRVKSKKLGKNGSGREPVEPIVLRNRPFRPHHSHRSGSKIS
VKTLKDSQPQQIPLQPLQBEGLAIEIEKKESDSESLPOLQPAVSVSSSTKSNRDRBEEA
KKKNKRSENTEISNQHSKHVOKENTDEOKAOLQAPAOEVQTSVPVQASAPVQNSAPV
QTSAPVEASAQTPAAPPLIKHTSILPPRLKTPADVKPKDPKNSPVQFTDSAPGFPLPLL
TVSTVIMFDRHLPINVERAIYRLSHLKLNSKRLGRQVLLSNFMYAYLNLVNLHTLYMEQ
VAHDKBQQQQQQQQQQ

>YNL112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACCTGTAGAAATCTAAGTTTACTGAAAAAATCAAGACGATGA
GATGTTACGGATCGACTCAAGACCCCTCTGCTACTCTGAAATTTCTAATAATTTATGCACA
CCACCTAGTATAGATACAGCTTGTATTTGTATCCCGTTTATAGTCGTGCTATTTAAAA
TCTATGATATAATACAGATAAATAACACTTCTGTACAAAGTGCTAATAATATGTAGAG
AATTCGAAATCTCTTTTAAAGCGGATTCGGTATGAATGAATGTAAGAAAAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTACCGCGATCTCATCGCAGAAAAAT
TTCTCTTCACTTATTTTGTCTTATAAAAAAGACTGCTACGCTCAATTAACATTTATATTT
TTCTCTATCTCAGTTATTTTCTTCTGTCACACCTGTAACAGATTAACAGCACTATT
AAGGCAATTTAGAGCAATAATGACTTACCGTGGTAGAGATCAGCAATATAACAAGATA
ACTACAGCTTAGAGTGGCGACTTCGCGGTGGAAGAACTCTGATAGAAACTCTTTTACA
ATGACAGACCAAGCGGTAACTACCGTGGTGGTTTCGGTGGTCTTCCCAATTTTACAAC
AACCAGGAAATTTGATCAAAACCAACTGGGATGAAGAAATTAACCAAAATTTGCCAATTCG
AAAAGAATTTCTATGTTGAACACGAAAGTGTTCGGACAGATCGGACAGTGAATTCGTC
AGTTTCAGAAAGGAAATGAATGACTATTTCCCGCACAGATATTTCCAAAGCCCAATCACA
CTTTCGATGAAGCTGGTTTCCCACTACGTTTCCGACAGATATTTCCAAAGCCCAATCACA
ACAAACCAACTGCATTCATGATGACGGTTGGCCAAATGGCTTTTATCTGCTAGGAGATG
TTGGTATTTGCTGCCACTGGTTCGGTGAAGACTTTGTCTTATTTGTATACAGGATTTGCTC
ATATCAACGCTCAACCAATTTATGCTCCAGCGATGACCAATTTGTTTGTGTTTGGCTC

26/251

CAACTAGAGAAATTCGGCTGTTCAAAATTCAGAGATGTTCCAAAGTTTGGCTCATAGTTCCA
GAAATAGAAATACCTGTGTCTACGGTGTGTTCAGAAAGATCAGAAATTCAGAGATTTAT
CTCGGCGCTGGAATATGTATGTTCTACTCCAGGTGACATAATTGATATGTAAGATTTG
GTAGAGCTAATTTGAGAGAGTCACTTACCTGGTTCGTGATGAGAGCTGATTAAGTATAG
AATAGGTTTATTTGAGACCAATCAGAAAGATTTGATCATAATCAGACTGATAGCAAAA
CCTTGATGTTGTTGCTCCACTTGGCCCAAGAGGTGAGCACTAGCGCTGATATCTTGA
AGATGCCAATTCAGATTCAGATGTTGTTTCTAGAACTATCTGCTCCCATTAATTTACTC
AGATCTCGAAGTTGTTTCTGATTTCCGAAAAGAGATGTTGTAACAAGTACTTTGAAA
CAGCTCTCAAGACAGCAATTCATTCCTTCTCTTACGAAAAGAAATGTGGC
ATGATATCCAAAGATATCTAAGAGAGATGAGATGAGGAGTTCGCTTACGATCCAGTACA
AAGACAAAGAGACGTGACGTGGTTCTACAGAGTTTGAAAGCTTATCCCAATTTT
TGGTGTCTACTGATGAGTGGCCCGCAGAGGTATCGGATGTTAAATTTTCCATTTT
ATTGATTTTATTTTATTTTGTATCCCTTACGATATTCAGCTATTTCCATAGGCTTT
AATGACATTTATGACTTTATGCAACAGATATGATACAGAGAGAGACCTTTTCTTTT
TTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
TCGAATCTAGACTATGATGATCTATTCGATGAGGAGTATCGGAAATTTGATTTTAA
TTGGAATGACTTCTAATGATCATACTACAGAAACTAATATTTGGAGAGATGAGAAAATTTG
ACTTTAATTAATGCTGTTTGAAGAGAGGAAATTAATACTGGGAGATGATATTTGTT
CATGATTTGCACTTCATCAAAAAGAAATTTGCTTTTACATCGGCGCAATTAACAA
GGAATTTGGCTTTGAGCTTATTTCTAGAACGATACATACGCTTGTGATCGTTGTTT
TTTCAATGCTTTGGCAATTTGTACAGGGTATGTTTATTTGAAAATTAATATGATATTT
CTACTTTGAAATTCGGCTATCTTCTGATATGCTTATCTCATTGTTTATAGAGTTATG
CATTTTGTGATTAATGAGATATCTGTGATCCCAAGTTGATGATTTTATAGAGTTGCTG
ATTAATAATGAAATTAACAAATTAATAAGATTTCCACCATTATTCAGAAATCATTTACTT
GTTTCTCTTTTCTTTTAACTGTAGCTTCTTCAATTCAGTTGATTAATGAGATTTGAGATTA
TGATTAATTAATTTGCAATCTTTTAAATAATTAATTTTCTGATATTTTCAAGCAAGG
GGAATTTGAGACATGTTGGAGTCCCAACATGATTTGTTGGGGGAGATGAAATTAAG
TTCAATTAACAGATATGAGTCCAAATTTACTACAGATATGCTTTGTTAACTTTGTTTCT
TCTTATTTTCTTCAATGTTCAAGATGATCAATTTAGCTTATCACTACAGATGTCAGAGTA
ACATTTGAGATTTGTTCAAGATTCGATGAGTGTGATGAGCAGTCTACTGTGATCTG
CTATATCTTTCTTCAACCGAACAACAAAGGTTTACGCTAAATTTATCTTATCATCA
GAGAGCTTTCTTCAAAATATTTCTCCCAATTAATTGAAATACGACAGAGATTTTANGTG
GCGGTACCCAAAGATACGGTGTGTGCTGGTGTGCTGGTGTGCTGATATGCGCTTACAGTG
GTTACGGTGTGGCCGTTGTTTACGGGTTAACGGCAGAGAGATGCTGCTGGGCTGA
ACAGAGGCTGTTCAACTATTGA

>YNL12W, 546 aa (SEQ ID NO 328)

MTYGGDDQYNTKNTKSRGDFRGRNSDRNSTADRPQGANVYRGGRSHSNYNQPOLIK
PMMDEDLPLPTPEKNTYVEHESVDRSDSEIAOPRKEMEMTISGHDIKPTTDEBAGF
PBYVINEVNAEGFDKPTGIGQGWPMALSGRDMVGIANTSGKUTLSYCLPGIWHIAOPL
LAPGDPPIVULAPTRELAVOIJOTESKFGHSRIKMTCVGGVPSQOIRJLSRSSEIV
IATPGRILIMLEKTNLKRVTYLVLEADNRLLDMGFEPQIRKIVQIIPDRQTLIMSAT
WREPVQOLADYINDPIQOVIGSLELSAHSNTQIVLEVVSDEKRLNKLKYLETASDNE
YKTLIFASTKRMCDITKYLREDGWPALAIHGDQGRBDMVLOEPRNGSPIMVATDVA
ANGIDWKNVIVINVDMEGNIEDYVIRIGRTBAGATGTALISTFTDQNKGLGAKLISIMR
ENANQNTPELLKTYDRSTYGGGHPRYGGGRGGRGYRGGYGGGRGYGSGNRQJHDGWMN
RGHSNY

>YNL131W, 959 bp, CDS: 501-959 (SEQ ID NO 329)

CAAAAAGAGCTAATCACTCTTGAACCTAATGAATACGCATTAATGATTAACAGTGAAG
GAATGGAGCTGAATCTCAAAAATCTTTAGAAATAGCTGCCAAGGCCAAAGCGTGTCACT
TTAAAACTGTGTTAAAAAGAGAGAGTGAAGGAGAGTGAAGGCTGCTTACTCTTTG
AAAGCTATGAAAAAACCAGAAAGTCTAAAAAGGCTGCAATTAAGGCTTCTACTCTTTG
TCAAACTCTTTTATAGCTTAACGTTTACTTAATTTGTACAAATATATATATGAAACAT
AGTTGATGTTTGAACCTTTACATATTTCTTTCAATGCTGTGAGAGATATATAGATTAGG
ATTATGCCGGGGAACAGTGAACCCGTTTGTAGCAATTTCAATCAACATACTCCACTCGCT

27/251

AGTGAATTAATCTTTTGAAGTAAATACGAAGTAAACCAAGAGGTCAAAAAGCACTAATACC
CCAAAATAGCAATCATTTCAATGATGTAATTAATTAAGAGAGTGTGCTCAAT
TAGAGAAACCAATTTTCCAGAAATCAGGCCATCGTGAAGAAAGAGCTTCAACAA
ACAAGAGCTTCTCAATGATGAAGTACTGTATAGTGAATTTGAAAGTAAATTTGATG
AAATGAAACATTTGTTGACAGAAATGCTTTTAAAGACATTTGCCCCAGATGAAGA
GACAACCAATTTCTAATTTTGTGTTTGTATGACCTTTTGTGAGAAATGCTTTACAA
AATCCGGAACCTTGTGAGACTTGTGACACACACTGCTTTGATGACGTTGTGATTA
CCTTATCTTACTTGGCGAACAACACTTAATCGAAATGAGAAAGACATTTGATTTACAA
GTGATGCTAATTAACATTTTGGCCCAAGGTGAAAAAGATGCTGACCAACGCCAATTA

>YNL131W, 152 aa (SEQ ID NO 330)

WELTEIKDVLQDEPQFSRNOIYEEKASATMNDVDEDDSDSDPEDENEETLID
RIVALKDVIYPPGRQPTISNPFQTSFVRNATFKSGNLAWTLTTTALLGLVPLSLIAE
QQLIEMEKTFDLOSDANNITLAGEKDAATATN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAATTAACACAGCGGAGAGCATATCAGAGGCCCAAGCAAGATTAAGACATGCTTTT
CTGGATTAACCAAGATTAATTAACGATATCTGGGACATTAATCCACACCTGCTGA
AGCCACAGCATCCATCCCAATGAGCCAGTCAATATGTATTCAAATCTGTTGTCA
CGAGTACCAACCCGTTCTTCCCTGCTGAGGCTACCTGTAATTTGATGAGACATTTGTA
TATTTGATTTGATTAATTAATTAATGATGATATTAACAACTAACTTTCTTTCAACCTCT
GTGACACTTAATTAATTAAGAGATATTTAATTTGAAAGAGCGTAAAGCAAGATATGAT
TACTACCCATGATGTTGTAGACATGATGATCTATCTGCTTATATATAGTCAGAGAAA
AGTGGCTCGGATTAACACCTTGTATGATGATGATGATGATGATGATGATGATGATG
ACGCCGCTGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG
AATTTACATTTCTTATCTTATCTGCTGATGATGATGATGATGATGATGATGATGATG
ACGACAGTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AAAAAATAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
CTTTCTAATTTTGGAGCGCCGGGTATTCGAAAGGAAAAAAAACCACACATCTCT
TGTTCAATTTACTATTAACAAAGCCGCTGCTGAGCGGCGGCTTAATCGTGA
TTTCCAAAGAACAACTTTAAACCGTCTGCTGAGCGGCGGCTTAATCGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MRBQKJLFTRELVDFTPLISGPDYQTLILISSNSKKRPXDSLSSEKKKKKKKKXDV
LSYSYLDLPFVPLFMQPGYSQREKMRQHSLEFIMTLIRKPMISWADMYVVSXKNSL
NRPAERGSNR

>YNL19C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGTTAATTTCAAAATACCTTATTCGAGAGCTTATCTTATTTTCAAGGCAAGC
TCTCCACATCGGTAAGTATGACCAATTAATTAAGTGTGCAAAAGTGTGTTGCTTC
ATACAGCCCGGAGAAACAGATGATGATTAATAATTAAGTGTGCAAAAGTGTGTTGCTTC
CCGAGCGCCCGGCTTCTCTCCCTGAAATCTTTGCTGCGGCCCCCTCTCAATA
CCGATCTGATCTATATACGTGATGATGATGATGATGATGATGATGATGATGATGATG
TTGCTTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
TCCTCCCTTAAAAAGAAATTAATAAGTATTATCTGAGCTTAATAAGCAAAAAAACA
CGTTTCGGGCTCGCTCAAAATTTTCAATTAAGCTTCTGCTGCAATACGATTAACGAG
GTTATGACGAATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
GTGCTTACTTGAATTAATCTCTCTCTTTTATTTCTTGATATATGCTCTTCTCTCTATC
TTAGTCTTGGCGAGTACTGGCAATCATGATTTCTCTTTTCTTTTCTTTTCTTTTCTTTT
TTTTTTTTTTTTTATCTTTTCACTTTCTGATTTCTGATGTTTCCATTTTGTGATTAAGTAA
GTTTAAATTAATGATCCCTCAATACAGCTACGCGCATCACCACAGCAACAAAGCAGAT
CTTGACCCATCAATGATTTCAAAAGGTTGGAACATTTCACTTTTCTTTTCTGCTTAT
TGCACAGACAAATATCCAGAAATATCACTTGTGATGAAATTAACAGACAGGTGGCACCA
CAAGCACAGCGCGAAATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

28/251

>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRLLCRQLSSAYLNYLPFYLIYRPSFLYSSCEYMQSCFSEFFLEFLFFRFFPFTF
QFLVAFPIILLFKVLSLNTLTKHVRPIHQRTKARSILTHCIPKRMNIHFPPFSGLLHKHTISR
IPSWIGNTRQVAPTKHPKYLLMTI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCAATTTCCACTGCTATTTCTGCTATTTGTCTAGTGTGACAAACCATTTGTTTACTTGAATGTTA
TTACACCAATTTTGTGATCAAAATATCTACTTCTTGTGGGAGACGGGTAGAAGATTT
GTATTTGGAGACGCTCTCAAAATATATGGCAAAACACCTCTAGATATTTCTAGTTTATTTCT
CATTCGCTCTCTTGAAGTCCCATTTATACAGTGACGACATGTGGTGTGCAAAAGTAGT
TGTCTTATTTGGATGTATCTCCCAATACGTTGAAATTCAGAGCTTTTCTATAGAAAT
TCTAACTGTGGCAGAGTTTCTGCTGACGTGCTGCTCGGCTCATTTGTGCACAGCTTT
TCTTGTGATGTGTGCAAGATAAATGCTTATCTGAACGTTTCTCTATTTGTTTTCGTC
AATTTCTTTCTTCTTCTGCTTCGGTTTTCGACATATTAAGCTGTATATAGAGAGAAA
AATGGCAGAGATGTACTAGATGATAAAAAATAATTGTAATAACGTTAATATATATAAAT
ATATCTATTTTCAATTAAGTTTATTTCTGCCCTCAAAATTTTAAAATTTGGGAGCAG
TCTGCTCAATGTGTCCTTTCAAGTTCTGAACTTGAACCTTAACAAATTTCTACTCTTTT
TATATCAAGAGTAGCAACGAGGTGTATGGGTAGCACCAGAACCTGGTTTCCCCACTG
GAATATGCTCTTTAGAACACGAGGAAGTCTCGTTAAGGATATCGAGAACATCTCGCATAG
TAAATCTGGCCTCCGATACGATAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MTKNNNVNIYKYLFYKFLYILPSNFKIWEAVSSVMVSKFNLNKPNNFLFLLSRVAP
RVLWVAPEGFGTGLPFRGKSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GGGTGAACATGATCATATTTCCGATTTTGGGTACAAATAATATATCATATATATATATAT
GTTTGCATGTAGGTTCTACAAATACATTTGTGTACGCTATAGTTTCTTTCAAAACCTAGA
AAGAATCTGTAAACAAATAATCTCCAATATTTTATAGCACCTTATTAATATCAATGCTGC
AATACCTCTATTTCAACAAATTTGGCCCTACCCTTTTGTGTACAAAAGCAAGCTGCCATTC
ATAAAATTAAGTAAGAAGCATATTTGGAATGTCCATTACGTAAAGAAAATAAATCATGT
TGTCATATATACGTAAATAGAAATACGGAATTTTCTCGCGAAGTAGATCTTTCCTCGGAGAAA
AAAGAAAAGATCCGATCAATATTTGAAAGGGGATCCTTAGTTTCCCACTATATAGGA
GGAATAAGCTATCTCTAGGCTGTGATATAGCTGTACGATACGATTTTCAACAAACAGATAGC
ATATCACACGCCCGTAATATGATGATGTTTCTGTTTCAAGTGTCAACCGGTTTCAATTTGCC
AACATTTGTGATCTCTGTTGAAGGAGACTAATAGGTATCGGTTCTGCCAGAAGTC
AAGAAAAGGCCGAGAAATTAACGGAGGCTTTGGTAAACCAACCCAAAATTTCTCCATGGAA
TTGTCCACAGACATATCTAGCTGGAGCATTTTGACCATTTTCCAAAGCAGCGCAAGG
ATATCAAGATAGTTCTACATACGGCTCTCCATTTCTGTTGATATCACTGACATGAAC
CGCATTTATTAATTTCTGTGTAACGGTGTAAAGGAATTTCCACTCAATTAATAAT
TGGCAAAAGAAAAGGATAAGCTTTTAACATTTAAACGAAGATCTCGAAGCTTGTCTGAAA
GGGAGAGTTGCCAAAGTGACCCAGTATACGCTACTGTGTTTAAAGAGTTTGTCTGAAA
AAGACGCTTGGGAATTTCTAGAGGAGATAGAGACTCTGTAAATTTGCAATTAATCTGCCG
TTAACCCAGTTTGTGTTGTCGCAATGTTTTGACAAAGTGTCAAGAGCTCAATTTAGTTGCCTTCC
ACATATTTGGGAACTGTCACAGCTTGAATGCAATTTATCACAGGACAAAGATACCGG
ACATATTTGGGTACATATGATGTGTGATGTGTCGCAAGGCTCAATTTAGTTGCCTTCC
AAAAGAGGAAACAAATTTGGTCAAGACTAATCGTATCGGAGGCCAGATTTACTATGACGG
ATGTTCTCGATATCTTAACCGAAGACTTCCCTGTTCTTAAAGGCAATTAATTCAGTGGGGA
AACACGCTTGGTGTACCCATACACCTTGGTGTACTCTTGATATAAATAAGAGTA
ACGAATTTGTAGGTTTCAAGTTTACGGAATTTGAAGAGACCATTTGACGACACTGCTCC
AAATTTTAAATTTGAGGGCCAGAAATATA

>YOL151W, 342 aa (SEQ ID NO 352)

MSVFVSGANGFIAQHIVDLLKEDYKJGSARSQEAENLEAFGNPNKFSMEVVPDLSK
LDAFDHVQKHGDKIKIVLHTASPPCFDITDSDRDLILIPAVGVKGILHLSIKKYAADSV

29/251

RVLVTSYAAVFDMAKENDKSLTFNEESWHPATWESQSDPVNAYCGSKKFAEKAANEFL
ENRDSVKFELTAVNPVYVFGPQMFQDKDVKHLNATSCELVNSLHLSPEDKILPELFGYI
DVRDVAKHLVAFQKRRETIQRLIVSEARFTMQDVLDTLINEDFPVLKGNIPVKGPSGAT
HNTLGATLNDNKKSKLLGPKPRNLKETIDDTASQILKPEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGTCTAGTACTACACGCTCTCTGCACATAGAGAATGAT
CCATCTGTCTTGTCTGCAGCAGGTTTCAGAAATCTTCTCTCGTGGGGCTCAGCAAAATGATTTG
TTATCCAGATCTCATATATGATATAGGTATACGCCGAAGTCAATTTCTCAGAGAGATAGAT
GGATTCAGCTAAGGATGATACGCGCAAAAAAATATAGATCAGCTTTTCAAAAACAACTA
TTTTGGCGTTTACCAAAACCAAAACAGATATATCAACTAGTTCAATCATCTTTGAAAACG
TCCCTTCTTCTACAAATTTAGCTTTTGAACGGTGTCTATGGAAGAAAGTGTAAAGAAAACG
AAAAAAGAGAAAGTCAATATATCTTATAACGAAATATACAGGTGTTCGACATCAATCG
CCAGGTGCCCTAAACAATCATATAGGATAGTCGGGCAATATATACGGTTCAATATAGTCA
TGAAGTGTATACAGAAATATGAAAGCTTCAAGGACTACAGGATTTAAACACATCA
AAGCGTGTATTTGTATGATGCTGACATTTATGCTTACCCAGCCTTGGATCTTTCCAG
CAATGAAAACCGCAATAGGAATGGAGGACAAATCGATTTGATATCTTCTTCAATGATTA
CATTGCCACAGAACCAAAAAAGAGAGCGCATAGTAGAATAGAAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCCAGCCTGCTCTGGTTGACATAATAGAGATTTTGACGA
AAAAAGTATTAGCAAGACATATGTACTAGAAAATGTCGGAGCCCGGTAGAGACTTTTGT
TTAAAGATTTTATTTCCATCCGAGCTTTTCAGGTTTGAATATATTTGACACAGGAGTTTA
GGCTTACAAAACCGCAACCAACCATTTATTCACATACGCTCCGGAAGCTTAAATATAAGGC
CCTTGGAAATGATCATGTAGGAGATTCATTTGACGACATGAATAATCCGGTAGATCTCTGT
GATGTTTCAAGGTTTACTCAAGAAATCATGTGAATGACATTTTACTGCTCGAACATTAAG
AACTAGTAGACGTTTTCAGTAGAGGATCTTTCCGAAATAATTCGAATTTGATTTCAAAATATGA
ATAAAGAAAGTTTCTTAA

>YOR131C, 218 aa (SEQ ID NO 360)

MYKLQDRIELHVKAAKEMQPPQGLVDIMRVLTKNGISKNICTRNVGAPVETFKRFIPS
KKEAHLGIELHVKAAKEMQPPQGLVDIMRVLTKNGISKNICTRNVGAPVETFKRFIPS
ELSRFDYIVTREFRPTKPPQDPLHLHASKLNIIRPLEMINMGVDSFDDMKSGRSAGCTFVLL
KNHVNGLHLLLEHKLVDVSDVLELSEILIELIQNMKNESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTTGCATATCTCTGCTTCTCATCATGTCCTCATATAGATCGCAC
CTGACCCATTTTGCCTTAGATCTTTAGAAATTTGAGAAACAGATTTGGCATCCCAAAACCTG
ACAGTCCCAAGGAGCTAATATTTTATTTGTGCTTCTTGGCAAAACCGGGGGAGAACTCAA
AAGTCGCTCTCACATGATATTTCAAAACACCTCACTATATCTCTGCTCTATGTAATGATT
GGGTTTCTCATGGGGGTAAACCTTATAGCTTATAGCTTGTATATCTCTAGGATGTACCC
TGCTATTTTTCGTAAGCTAGTAACTGATATATGCTCATTTATGTCACACCGTTCAATAATT
TGCTATTTGCTGTGTATAGCGGCGCGCAAGAAATTAGGAAGTATATAAAAAA
AATACAAAACCTTAACTGAAATAGATAGCGATAACTCTCAACAAATGGAAGCGAG
ACAGAAAAGAACCAACGATTTCAAGCATAGTACAGGTATCTCTCGAGGACAGTTT
CTGCAAGATCGCTACATTTGCTCTGAGAACATTTTACACGAAGGCTCCCAAGATCTATA
CTTTTCCACAGGTGAGAACCTAGTTCGAACACCCCAATGATATAAAACTATTTGGTAGTG
TAAAGGACCCCAAGGAAGTAAAGGATTAACAGTGCACCAATGATAAATAATTTGGTAGTG
ATAGTCCCTTGGCGCTCTTGGATTTGCCGAAAAGAGGTTTCAAGATTTTCCAAATTTG
CTAAACCACTCAGATAAGAAATGATTTTCTTGTGCGAAAGGAGTAAAGAGCCAAA
CTGCCGAAGAGTTGGCTCGATCTTTATGGGTACGAAAACACTGGTATCTATCTCTGTTCTA
TTTACTGAGTGGTTAGCTAAAGGTGGTGTGCTGAGCTTAAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MPKHSHTGILLSRSPTLVLRFTTTKPKIYTFDQVRNLVEHPNDKLLVDVREPKEV
KDYKMPPTTINIPVNSAPGALGLPEKHFHFQFAKPHDKELIFLCAKGVRAKTAELAR
SYGYENTGIYPGSITEMLAKGGADVKKPKX

34/251

[illegible]

>YPL190C, 802 aa (Seq ID NO 388)
MDENNNISVDIIPSPELSTYNSNENLENNMNSADGIEFDAPBEERBEAREEENEECH
ELEVDNDEEBEEKEBKEBNGEVINTEEBEEBEHQKGNDDDDDDNEEBEEEBEEDDD
DDDDDEEBEEEBEEKEBNGNSVGSDEAADEDEEDKDYKQVELARETILEKQK
DYDEAIKKTIREENDNTHFNNMEENVNDLQOKVYIMDSMTNLPOFQHPQEKSA
ILAMLSNSPTALSVPRDSTITSTTASASATGASANDQKRPUSDAGRMFPKADSL
PITEEBEHDRAVYAHGENKTEEMHNIPEKSRITGNLPKRVSKSDLRIFSPYGHIMQI
NINAGEGFQIDNFOVSVDALIECSQEMNFKKLLLEVSSNARQPFHGDGNTSSFFN
ISSAKRPFQESGMDLNDAGYKYSRRHTVCSIKFKRTDGTALTEVFNRPDGTGL
ETDMILPKPMEELKLLINDAAVNGYGVSVLVNKTNVNDQFYKSGQGTETDEYISTISA
DDVAIFENNIKNNNNNSAPDTYRAASHOONIGAPRLPVNGPANGVPPQNTYVGYSNM
PPOQOQOQPYGNTYGMPPPSHQGYESQPIPNMOSAGVOTSIPIPPPOOQIPQGGRYG
ACGPPCPSPSTPMQOQLSLAQNLPIPNVNVLSMAQQOQOQPHAQOQLVGLIGSMGQY
APQOQOQOQLGYSYSSMSSSPPMSTNYNGNISAKRSPAPPMQOQOQOQOQOQOQ
QOQOQOQAGNTVQSLSSDKLQK

>F01201C.1886 bp, CDS: 501-1886 (SEQ ID NO 389)

ATTTCATCATCTAGTATGTTATTAAGAAAGAGTCCCATCGAGGAAATATATCATTTCT
TTATGTGCTTAATTTCTTCCAAATGACATACATGACAGTTCCATTCACAGTGC
ATTGTGGGACACAGCTGTGATTTACCTCTCTGTTATGGAACCATTCATCATTTCTAGT
TCTTCTTTCGCAATATTGCCCTTTGGGAAGAAGATGCAAAAGTGCATTTTGATGATTA
TTTTTACTATTTATTTCTGATATTTCTGATTTGCGGGCTAAAGTTGCCATTTTATGATA
TTGCAAGCTCAACCCCGCATTTCCGAGGTTTTCTTTTATTTTATTTGGGTATTTTGGAG
TCGGGCGCTAATGGGTGGCGCGGAATGCTGACACACTTGTAATATATAGAGAAATCC
TACATGTGTTATAGCAAAATCACAGGATATTAATGTATTTGCTCAACACCTTCAGAAAG
AAATATATCATACGAATATCAGATATGGGTATCTATAGCAATATACAGACAGTGGAGG
TGCAATTTTACACGAGATATGATGACAGCTGATTAATGGAACGAGTAAAGCAATATGAC
ACTACACGGTGAAATATGATTATCCACAGCTCCGAGATGACATTAAGCAATATGAC
ACCTACCTGTACCAATGTCGAGAGGTGTTGGAGATTTGGAAACTATTTCTGAAGAAG
ACGTATCATGTGACGAAGAAGAAGAACTGGAAGATGTTTGTGCAATTAACCTGGGTGG
AAGATTCAGGATTAATACATATTTTACTACCCAGATTTACAAATTTCAAAAGTTTAA
GAAATTCATATACAGACTACGATTTGATTTTATTTATATACAGCAATTTTACCGGAGT
TCTGTATAGCTTTTAAAGGCGCACATTTGATTTTATTAAGCAATTTTACCGGAGT
TGAAATTTAGCTTTTAAAGGCGCACATTAATGATATGATGATGACATTTTGTATTAATCA
ACCAATTTACCTTTATTTAGTTGATTTGATTTGAAATGGAAGTTTAAAGTCAATGCGCAT
ACCACTTTCAAAATTTTATTTAGTTGATTTGATTTGAAATGGAAGTTTAAAGTCAATGCGCAT
TGAAAGGAAGCTTAAACATATCTGCTGTTTAAAGGATCTTCACTCTCTATCAAA
GCCACCTATCTATTTAATATCTCTGGGAGATTTTAAAGGATCTTCACTCTCTATCAAA
GTTTAAAGATGGGCTGTATTAATCTTTTATGATATCACCAACAAGCAATGGAAGTTTTC
AAAGTTTCCATCCCAACTTGAATTTGGCTGTAGATCTAGCAGAGCAACCAATGTCAGT
ACCTTTTAAATTTCCCTGATGTTTACTTATTAACAAGAAATTAACCTTTATGCTTAAAA
AGATCTTATTTAGATGCGATGATTTTCACTTAAACAAGAAATTAACCTTTATGCTTAAAA
TAGACGAAGAGTTTCAAAAGATGCACTATCTTCTTAAACGAATATCAATTTCTTCTC
CCAAATGAGATCTGTCGATTTCCCAACAAGAACCCCAATGAGAAATCAATTTCTTCTC
CACCGCTTGACAGACGAGGTTTATCCAAATTTTATTAAGACACCAAGAACCTTCAATGTC
ATGCTGTAGGAACAGAGCTGATAGCAAAACAATGGAAGTATATTTTATTAACGAGC
AACTCTCTACGGAACAGCTTATGCTATTAACAATGATCTCTATCTTTTCAAAAGGTGGC
TTGTTGCGGCTATCTACCTGTAATTTAGGCCAAATGCGTATTAAGAGTCTCAAGATCTCT
TTGTTTGGTAATGTCCTCTCTGTAATTAAGCCAGTGGACAAATTTCTACTGATGACAAATTA
ACATTCAAACAATCTTCTTAAATTA

>YPL201C, 461 aa (SEQ ID NO 390)
MGIPIQIYQDGGVQVYFHRYYQVWPEFRASRKYNTYNNIYFQLEPDTLKEHIDQLFISVY
GEDGDVDVANYSEEDDDEKEHLEDFVRSRNGLEFVRLNNYFTTHDLOSFKSPRRNSKY
WIFYSNQLQEDKLKLDVFNQGHILFTRQCYGYQLNLISDAICMDCNFGYNSNTQIIV
GFQNGRLKLNCLNGLNANNHLLKRPSTSHQSHLSTLNWAGLLPHFVRSRLDGLD
ITSLDHQSGNGSEFQSHYINDLPEVDLTFTTNVSKVLNPOFLYKGNDAIFPKKMLGSD
ASTLKEINFEMLKIDEDVQKIDPLKTNHLLLENNRRLAIFTRPIIDNINSNPPVSDSE
VYPIFYKQGLLHVHVASGTQGLANNNGYIIFTECHLYGTALSVYKYSISFKRLFVGYSD
IRAKYGIIRSVKDLFVGNCSVNSPVLTLPDDNNIQTLFLK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2: 685-1176 (SEQ ID NO 393)

ACAAACCCGTGCATCTCCGAAAAACAAAAATTAAAGCTTGAGAGACCTTCAGAAAGA
GTTCCTATAGATAGATGGGTAAAGCGCAATTACTAGTTACGAGCTAAGTAGATTATATGCG
TGCTGAGGGGACGACTGACTGTTATATCAATCCGATTAATCTTCCCTCTGAAAAAAA
AAACATCATCAGTCAAAAGATTTTCTTCACTCTTTGGAAGGCTGTGGGACATTCGAA
CCTTATATTTTATATACCAATCTTCGATTTTCGGTGTCGCTTCTTACGCGCGTATAT
CTCTCTCTTGTCCACGCTCAAGGAGATGGTAAACCCCTTTCAAGTTGACGAAAA
AAAAAAATATGTCCTTCAAAATTTTATTTGATTTAAATTAAGTCAATCCCTCGAAG
CTTGTTATTCGGAAGAAAGATCTAAATTTTCCAAATGGTAGAGAAAACAATTAACAAA
GACATTAACCCGACCTCCATCTGTCCTGAATAGCATCTAGATTACATCTCCAAATGAAC
AATTCGATACCGTAGTAAGATGGTTTATATGGTCCATCGTCATCTATGTTCAACAGC

38/251

TTACATGATGATAGGCGTAAGTCTACCGCCACGTCACAAATGACATTGACCT
TTCCTCATTTGAACCTATCAACTCTCCCAATTTCTCCATAGTTATTT
ATAGAGAAAGAGGGGACCAATGACGATATGTAATTTCTTCCGACATC
GATCATCTTCCATCGGAGATGATCTGGATAGCTATGTAATGAC
CAGATGATCAAGCCATATTCAGTCAATATTTGAAAGGAGGAGCTCA
AACGATCCCTGGAGACTTTTATCAACGTCAGATGTTTAACTGTAACGTA
GATAGCGCAACTATGCTCCGCTCCAGTCGACACCAATCAGCAGCTGC
AATATCAAGAGCTCTGCGGCTCCAGTCGACACCAATCAGCAGCTGC
ATTCATATGAAATCAAGCTATTTTAAATGACCAATGAGAAATATGTGAT
AAAGTCTTAGATACATGAAAGGATGACATGATAGTAGTAGAGTGT
CATGACCTCTATCCAACTTCTCTGTCGAAAGATGTTAATGCCACATG
TGAGGAAATGAAACGAATTTATGATCTTTTCAAGATTAATTTCTTCC
CATTTCCCTATTTATCCAGCTGCTGCTGATTTGATTTGATTTGATCTT
GCACGATATCTAATGAGGATGGATGATGACGCTGAAACGCGAGT
TGTTGATGATTAAGTCAAGGACAGATTAAGAAATGATGATTAAGGAC
TATCAATCTTGTCCATTTGAAATGCTTTGTTTACCTTATTTATGCGC
CACATTTGGTCTTTGATATGTTGCTTACAAATCTCAACAAATGAAAT
TGATGAGATGATGAGAGATCAACAGTAATGACATTAACAAATTTGGTAT
AGGTGTCGAGTCAACAGTAATGACATTAACAAATTTGGTATTTGG
GCAATCCCTATATTTGATGATGATGATGATGATGATGATGATGATG
AGAAATGATCTCTTTGATGATGATGATGATGATGATGATGATGATG
ACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TATCATATATACAAATGATGATGATGATGATGATGATGATGATGATG
TATCATATATACAAATGATGATGATGATGATGATGATGATGATGATG
CAGTTCTTGAATGTTCTTCCATATTAATGATGATGATGATGATGATG
AAAGATGTTGAAACCAATTAATATTCGACATGATGATGATGATGATG
GTGAAATGATATATGATGATGATGATGATGATGATGATGATGATGAT
GATTTAGAAACCTTTTATGATGATGATGATGATGATGATGATGATGAT
ACCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT
AAGGACCAATGATGATGATGATGATGATGATGATGATGATGATGAT
GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATTAATAATGATGATGATGATGATGATGATGATGATGATGATGAT
AATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAGTTGAAAGGACCAATGATGATGATGATGATGATGATGATGATGAT
TGTGAGGTGATTTTGAAGATGATGATGATGATGATGATGATGATGAT
TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
CCAAATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT
TTCATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT
GATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATGCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTTGAATCTTTTATGATGATGATGATGATGATGATGATGATGATGAT
TGTGAGGAAAGGAGATGATGATGATGATGATGATGATGATGATGATGAT
ATGTTACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCATCTAAAGGAAACATTTGA

YDR216W, 1323 aa (SEQ ID NO 110)

MANTEKPNDCGFPVVDLNSCTSNCPNNKEQIEHMETDDSPILIMSSAS
RENSNTFSVIQRTPDGKLIITNNNNNSKINQDLKLEMLRATGRTPSGK
LRSFYCEVCTRAFAQEHKRIYRSHTHNEKPYPCGKCNCFRBRDILLRH
AOKIHSNGLERTISHTKRVSRITIKARKNSASVKEFQTPYGGPDNENFL
NRTTANTRKASPEANVARKYKLUKLTBRASFSQASASVAPQSSLEOH
PKDRKFTSTPELVPLDKNPBELDSFPLNNDLNDLNLSDNENFALNRSD
SSGSTMNLDYKLPESANNYTSSSGPTRAYGANTNSKXASFPNDLLSS
SWIYAVNDHLFVSSESDTSPNSSELNDTKLVPPFKSTIHLKDRSS
SWTVAIDNNNNNNKYSDNQPDVVDQELDNDLNDLNDLNDLNDLNDLNDL
LHDDSVSATATSENEIDLSLNSPISPHKLITYKXKEGTNDMLISFGL
DHPNSREDDLDKLCNTRVQALFSQYLAKESKRLSEDLSTNRKEP
DSGNVTYGLDCLTSKISRALPASTVNNNQPSHSIESKLFNEPRNKCI
KVLRYEKFSDSHSSESVDSNENPLSKELMPVSELENEYLDLKFNNFLP
HPPIIHPSLDLDLDSIQRYMEDGYDAENAOULFRLSQGTDEYDYEH
YQILSKIVCLPLPATPGSLHKPGYKSGQITELYEMSRILHFLFETKR
RORSTVNDVYONIMQSLILSFMPALVADYLEKIDLSLMKROLALCS
TIRSNCLPTISANSEKINNNEPLTFGSPLOYLIFESKICRTMAVDPC
OFLKCPFHILKFDLSIEKDEYETIYPDNESKWASESIIICNGHVQKQNFY
EESLDSSYNDNMAATNNKIALIDDTILKNLMSKRFIKQIDRSTPE
KVRKQIATKYIDFSLNSVRNPLKNVSEVLECEFLVAFNLSIRNLSLV
EESLDSSYNDNMAATNNKIALIDDTILKNLMSKRFIKQIDRSTPE
NPLVGLRIPIELASLANSILLPTLSRLYPOFSGPVDVFTQFINKQNG
MLVPGLSANHHNGASAAVTKLAKINBELAMFINELIVNSFNDSTPL
NMEDPIINERFSFNDGDAVTDLPSSAHLISDTGLEGINFSGNDSHQYVS
TJNLRLRGENHSSKHNGKGGQGFPAEKYQLSLKYVTIAKLPLTNVXENYI
HCHMDKMAIDFHTLENHLKGN

YBR112C, 3401 bp, CDS: 501-3401 (SEQ ID NO 51)

GGGCGCGTATCGGCTTAATTTATTTATCTCTATTTCTTCTTCTTTC
TGTGCGGTACTCTTCTGATCGTGTCTACTCCGCTGACCCACTGCG
TCTCCCGGATCTACTCCATCTTTTGTGGCTTTTCCCTATCCAA
CTGCAAGAGGTGTGTAATTTATTTATTTCTTCTTCTTCTTCTTCTG
TCTGTTCTTCTTCCGATTAATCAAGCAAAAGGCACTTTTCTTCTG
TCTTTTGTTTTGTTCCTGTTCTGTTCTGTTTCTTCAACACGCTGAC
GAGTTCAATTGAGAGAACTAGAAATCAACAAAGCAATAGCAAGCTCA
CTAGCTTTGAACGAGCGGTATTCCTGTTACCTCTTCTTCCATATTC
TGTTTCTTCTTCTGCTGATTAAGCTTGAAGCTGATTAACATCA
ACACCAACACAAACAAACAAACAGCTGGAAGAAAAAATAGGAA
ATGAATCCGGGCGGTGAACAAACATTAAGCAACACCGCTCAACGCA
ACACCAACAGCAACAAACAGACAGCAACAGCAACAGGCGACGCTTC
CTCAGACGCACTGACCCATTAACAAATCACTGCGGAACTGTGCTC
TTCATGTCTTCTTGGCAAAACCTTGTGTGATGCGGACAGGCGCAAT
GGCATATGACGCGCACTTACAGTTCATCTTCATCTGCAAGGCTTTAA
CATCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT
GAATTAATGAAAGACACTTTGTGTAATCCGAACTATTCAGATGTGTG
GGCTACTTATGATGATGATGATGATGATGATGATGATGATGATGAT
ACATGCTATCAACAGGCTCTTACCACTCACTGATTAATCCCAAGTACG
AAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTATGCGGAAAGCTTTTGGCAAGTTTGAATGGAATGACCTCATTTTG
AAAGGCAACAGAAATTTACTTCAGACTAGGATATTAATTAACATGAG
GATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTGCTCTCTTGCAGAGATGGAAGCAATATGATGATGATGATGATGAT
TGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTGCTCAAAATCAATCAATGCAATGCAATGATTAACAAATATGATGAT

40/251

TTACGGTATGAGTAAAGCTAACATTTTATATGACCCCTCAAAGGCCATTTGATTT
ATCTTCTAAAGCTCTTTAGAACGACAGATCCCTCCGATGACGCACTTACATGATGTAC
CATCTCGGTGAGTGCATATATGATATCCAGTATCAATATATCTCCGCGCATATGA
TGCTTTCCAAACAAGCTCTTTATAGAGATTAAGAAACCCCTATCTTTTGGT
GCTCAATCGGTCTTTTATTTATACCAATTTCTTCAATATAGAGACGCGCTTA
GACGGTACACAAGAGCCATTAAGATTAATATCTTTATATTAGTGAAGTTTG
GTACGATCTAGGTACTCTTTACGAAACTTTGTAACAACCAATATATTCTGACG
CCCTTGATGATTAAGACAGCTGCGAAGCTGAGAGTAAATATATGTTGCAC
ATAAGAGAAAGATTAAGAGCTTTTACAAAGCACTTAGAAACACCCAGCGAA
TATAAACAATTCGAACGGTGCGCAACGAATTCGCTCTCTCTGCCCCACCTC
CTGTGATTTTACAACCTTACTTATCAACAAACGCTTATTAATCTTCTGCAACAATGT
AACCTAGATATTTAGCCCAATATCTGCCAATATGCTTCTGCTCAATATGTTAT
ACAGTATGGAGCTTCTCCCTCAATTTACAAGCTCAAGCTCAAGCTCAAGCT
CAAGCAAGAAGCTCAAGCAACAGCAAGCAAGCTCAAGCAAGCAAGCAAGCAAGCA
ACGCGAAGCAAGCAACAGCAAGCGGGAAGCAAGCGCAAGCAAGCAAGCAAGCA
CACAAGCACAATGCAACGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA
CAAGCAAGCGCGCGGCAACACAACAACAACAACAACAAGCAAGCAAGCAAGCA
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
AGCAGCGAGCAATTTACAGCCCTTACCAAGCAACAAGCTCGACGAAGAAGGGA
GTTTCTGCTCAATATGTTTAAATCTTCAACAAGGCAACATATATACACACA
GCCAACAGTCAATACAGCTACCACTTCAAGCGCAAGCTTCTTACACAAGCTA
TGGAACATCCGCAAGCTCTCAACTCGCACTTCAACAGCAACAACACTACAA
TCTGTTTCAACATCTCAACACACTTCAAGCGCAAGCTTCAAGCGCAAGCTTCC
CCAACTTTTATCCAGCATTAAGCTGGAACAGAACGTTCTCAAGCTTCTCAAGA
GATACATGGAAGGTGATCTACACACTTATGATAGATGTCGCGCTTATCCAGT
AGCACCCACACAGAGATTAACAAGAATCTCTCTGCTCAACCAACCCCATGCG
CATTTCAAGCAAGCTCCGCAACAGAAATTAACAAGCTCTGCAACCCACAGG
TAATGACGCAAGAAGTTGAACTCTTCAATTAAGAAAGATGCAATCTGAGGTGAGCAACCA
NATACTGCTTACTTCTCAATGAGAAAGATGCAATCTGAGGTGAGCAACCA
ATCGCCGACGAGTAGTGGAGCTTAATACCAATTAATTAATCTTCAACAAGAA
AACCTGTAAAGCAAACTCAATTAACCTTCAAGTAAATTTGGCGCAACAGAGACCT
CCACAGGAAGCTAGTCTCTGAGAGAGCTTACCAAGCAAGCTTCTGTTGTTTC
CTCTTCTACAAACAACCGTTTATACGGAACCAAGGCTCATCTAGTGTCCAAAC
CAACTGTATCATCAGAAAGTTTCAACAACAAGCAAAATGACCAAGACACT
GCTGTAGACCAATAGAACTTTTACTGCTACTGTTCTTCTGCAAGAGCAAGGCC
TGTAAGACGAGAAATTAAGATGAGATGCGGAGGCAAGAGCTTCCAGAGAT
NAGCATCTGCACCTTCTACAGAAAGCTTCTTCAACGATTAATCTGTAATCA
GCTGTAAGAAACAACAAGATGAACCCGCTGCTTACAGATTAATCTGTAATCA
ACCTACTTTTGGAAACAATGGAACAACAGTAAGAGAGGAGGCCAAATATCGCTG
AGGAAGACCAATCTCTCAAGAAAGTTCCTCCCAAGGAGAGACACTACGATCCA
ACGAAGAAGCAATTAAGCAAGTAAGTAAGAGAGATGAACACTACGAGCACTCA

YBR112C. 966 aa (SEO ID NO 52)

[illegible]

41/251

[illegible]

YMR043W, 1361 bp, CDS, 501-1361 (SEQ ID NO 305)

AAGCTGTGCCAAACAAGGTCATCTCCAAATACTTACCCAAAAGCTGATGGCC
GTACTGTACTGGAAATCTCTGCTTTTTCCTTCTTCTTCAATTTGGCTT
TGTCTGCTTTTACGTCGTGTTTGGCGTTTCGCTTTCTTCTTTTATTA
CTCTGTTTGTAAATCAATTTTCTTAAGTATTAATACATCTATATCATCGCA
TACCCAAATCGGTTCCCTATTTCTCACCACCTTTTTCGAAAAATACATATG
CTTAACAAGCAAAATTTTATTTTACGTTTGTGTAAATTCATTTATCTGATTAAT
TTTTTGAATTTTATTTTGTATGACATTTTATATCTGCTTTTGTG
CTGTTTTCGATTCAGTATGCAAAAAAAGCGGAAGGAAGAAGAA
AAAAAAATAGTCGAGACCAATAGAACGGAATAATATAGCCACCCACAGCAAAA
GATCTGCAAGACATTTGCTGTACGCAACAATATATAGCCACCCACAGCAAAA
ATGTCAGACATCGAAGAGTACGCTTAAATATATGCGCAACGACAAAGA
GAGAAGAAGATATAGAAATTTAAGTTTCTACGAGATTAACAAAGCGCCCATG
TGACATTTTCCAAAAGGAAGCACGGTATCATGAAAAAGGCGCTTTGAGCTT
TCTGTTCTTAACGGGAGCCGCGCTGTTGTGTAGTCTTTCAGAAACAGG
TTTGGTATATACTTTCACGACGCCGAAGTTTAAACCTTATGTCACGACGAC
AGGAAGGTAGAAACCTGATCAGGCTGTCTTAAACGCCCTTGATGATGAG
GAAGAAGCAGGAGGAGAGACGGTATGATGATGATGATGATGATGACATGA
TGTTAATGATATGCAACGCCACGACACCAACACACGACCGCAACAAAC
ACAAACAAGTATGTAATGACACGGCAATATAGTTTAGGCCCATCTAAATCA
GATCAATGATCCGCGACGCGCTGAAACAGAGGTGAAGTACAAATTCCT
AGCGGTTGCCAATTCCTAATCAAACCTCAATGATTTCAACAGCAGCAACATC
ACACGCAATACCAACACCAACAGCAACAGCAACCAACAAACACAGCAGG
CAATGTCTACGACCAACAAATGTCTACACAGCATCTCTCGACCAACGACGAAGT
ACCACTCCGCAACCAATTCGACGCCACGACCAACGACCAACCAACCAAC
AACTGCAACAGCAGCAACGACGACCAACCAACCAACACCCCTTACCCGGCATT
CATCAGCCTCCCAACAGGCTTTTGGCAACGCTGCTCCCTCATCTCGAA
TGCTGAACAGAAATGCTGCTTACCAACATACTTTTCAAGAACCGCAACAG
GCCAATCTAA

YMR043W. 286 aa (SEO ID NO 306)

[illegible]

VPL089C. 2531 bp. CDS: 501-2531 (SEQ ID NO 385)

1FDDCG, 2331 bp, CDS: 502-2222
TTCACGCTGTCGCAAAAATATCTTCACGGTACGAGTCTGTCTCTCAGTCG
TATATTAATGCGAGAAATCGTCTTATCATATTTGGGCTCTCTTAACGGCG
CAGCATCACCGGTGTAATGTCCNAAGCCGCGAGAAAGAAAATAATT
TACTTCAGATTTGATTAATAATTAACCGAAGAGATGAAGCTCTATAAAT
AGAAACAGCTCGATCTTCTCTGACACATATATTAAGGACGACAGACAAA
AGAAACGCTGTAAGAACGACGAGCTTTCTTAAGTGTTCACGACTGAT
TCAATATGACATGCGCTCATCTGATGACCACTCAACTGATCTCGCTGTA
TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

42/251

AAGTAATTGAAAGCTGGCAAGCAGATTATTTCTTTTTCACAGTT
 TCTATACGTTGTGAGGTTATATCCCGGAGCAACAGCGTGAAGCT
 GAAAAAACTTAATTAATTAAGTGTCCAAAACATATATATGATACAC
 AAGGAGACGGAAGATTGAATCCAGAGAAATTTCTGATGACAGAAATG
 GCGTGTACAGTTTATTAACCGTAAAGCTGGCTTTTAAAGAGCCATG
 AACTATCCGTTCTTGTGCAAGTACATAGCCGTCATATATCTGAGTTC
 AATTAACAGTTTATGAGTTTCTCTGTGTGATGAGAAATGTTAACTA
 TCATACCAAAATGACAAAACCTGCTTCACAGAGTGAAGATCTTCGG
 ATTATGAGACTTTACAAAAGTGCATCCGTTAATCAATATCAAGACTA
 CTGAGTGTCTATGTCAATTAAGCTTCGAAATCAATGTTAAAGAAAT
 GAACCACTCAGAAAAATGATGATGATGAGAACATGATGAGAGCAGATG
 ATCATGGCAATTTTGAAGAGATTCAAAATGTGATTCGAATTAAGAAACCC
 TCTGATAAAAATATACCGAGTGCACAGATGAAGTGTATATCCCGACCGC
 ACTCATTTCAAGATGATGATGATGATGAGCAAAATTAACGTCACTGAGA
 ACGGCTGCGCCCTTTACAACTTTGAATAAGATGAACGCAAAATATATGAGAAC
 CAATTAAGTGAATCTCCGACAGCAACAGCAGCAAAATATATGAGAAC
 ATACCATATGATGATGATCAATCTTAACGACGCTTCATCCAGTTCACTTC
 CTCTCCACAGATGATTTTCCAAATTTACCAAGCTTTCAAACTCTTC
 TTTATATGCTGCTCTCCACCCATTTCCATTTACCGAAAGATTCACTAA
 GCAATTTTCAATATGATCTCTCAAGACCTTAAACAGAGACAAATTA
 ACAATATGAGCAGCAATTAATGATGACACAGCACTACACTGATGACAA
 TCTATCTTTGAGAGACTCTATTTCAAGACATGTCAAGCAAGCAAGAA
 ATTGTCCCGCCAGACCGGATCTGTGAGATTTCCGAACTGCTGCTCTCCACATCG
 GAGTAATTCGCTATTTCCAAATGAAACCTCTCTGCTCTCTCCACATCG
 GCCAAGGCAATGATGATGGGCTCTGCGAGATTAATGAAGAAACAAAC
 AAGTAGTGTACAAATAATTTCTCACTATCCGATTCGCTCAGAGGACCT
 TAAGTGTGTACAAATAATTTCTCACTATCCGATTCGCTCAGAGGACCT
 TAACTGTCCAAAGAAATATGAGCAGAAATGATTAATTAATTTGCCAAT
 GCAATGGGCTTAACGCTTAAACATATGATTAATGAGCAATTAATTAACAA
 TCACCTTATCTCTTCCGAGTGTCTTCACTCTCTTTTTCGACACAC
 TACCTATCTCTTCCGAGTGTCTTCACTCTCTTTTTCGACACAC
 TTCCACAAATATGATCTTTTTCGATGATGATGATGATGATGATGATGAT
 ACCAATGCTTTTCAAAAAACAGAGCCAAACAGTACATTAATCAATCAAT
 TAAACGAGCGCCCTTCACTTTTTCGAGCTGCTGAAACAGCAATGAGC
 TTAACGAGCTGTTCATGCTGCTGATGATGATGATGATGATGATGATGAT
 TTTCTCCAAATGTTTCTTATATGATGATGATGATGATGATGATGATGAT
 CCTCCACATGCTGCTGCTGATGATGATGATGATGATGATGATGATGAT
 TTTCTCCAAATGTTTCTTATATGATGATGATGATGATGATGATGATGAT
 CCAACATGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT
 GTACAGACGCGCTTAAACAGGCACTTCAGCAATATCAGACAGACTAA
 CAACTATTAACAAACAAACAAATTAACATTAACAAACAGCAGCAACAA
 ACAGCAACACGCGACAGCAATTAACATTAACATTAACATTAACATTAAC
 TATATGATTAATGAATGACCGGTAATGAGCTGCTGATTTTTCAGAAC
 TACTACCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 CTCTGTCCACCGCATTAATGATGATGATGATGATGATGATGATGATGAT
 ACTGCTTAAACACCACTAGGCACTTAATTTCTTTAATTTTTCGATGAT
 TTTACAGGAGAAAAAATTCACAGCAAAATATTA

YPI089C, 676 aa (SEQ ID NO 386)

MGRKLEIQRISSDNRNRAVTFIKRKAGLFKRAHELSTLCQVDIAVILLGS
 NMTFYERSSVDITNDLIYHONDKNILHEVDDPSDYGDFHKSASVINIQL
 LRSMSNKPSSKSNVKGAMQSENDDEDDDDDDGDNFERNSSNMGSKKA
 SDKNIPSAHMKLISPTALISKDGEONKRPENALPLIOLIKRLKDPDPL
 QISHTPQQOQONISRPYHSSMTNLNPPSSSSSPSTMDPKLPSFONS
 FNGRPPPISTIPNKFSPFTNASSRTPKQHKINNSSNNNDNSNVTQSP
 SNTSLEDISIQTVKARKLSARPLVLRIPMNNFSSNSAIPSEPSASSTIS
 ANGSMSISOIMKENKTSRSKSIPLSASASGPTLLQKNNGRVITKLPN
 ANAANGSNNGSNNNNHPYPRGSSPLFSATQPIATPLOPNSINPGP
 FQQTSTFLAQRQTQOYQOMSPKROSTVPLTTTLTGRRPSTFSPEISNG

43/251

PPTGSLPSKFTVHDLMSNSPNVSSISMFEDMSMGPNKAKDNTNNPGTFPP
 VQTAIVNNGNSSNISSTNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
 YSNNEADAPVNGAIAISEHTTDDGSDNNNSSTYDAAATAYNGTGLPYIN
 TAQPTLGTTFEFTDISEKRNISKI

YOR372C, 2165 bp, CDS: 501-2165 (SEQ ID NO 371)

AAAATCGTGTACTTTCATATTTCCCTTAACACCTTACACCTGTACTGT
 GCGCGTTCAGCGTAGCTTTCGTGTGATTTATTTGAATTCCTCAGC
 TGGCTCGATGATTTCCCTCCCGGATATCATATCATTTCCGATGATCT
 TTACTATCACTAGTGGCAATTTTTCACCTGAAATATTTGTAACAC
 TTTCTGCAATCTGATATCTGATGATGATGATGATGATGATGATGATGAT
 CGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 TTTGGCGTTTGGCGTAACTCCCTCCGGAAGAAAGAGAGAGAGAGAGAG
 AAAAACAACAAAACAAAGCAAAACAAACAAATAGGACAGAGCTTAA
 GGAAGCTGCAAGATCTTCTGATATTTGGCATATGAGCATTTGATCCACT
 AAGTGTCCAAATTTGATTAATTTGGCATATGAGCATTTGATCCACT
 ATGGAACAGATATTAAGCTACAGCAAAATTAATCTCACTGAGGCAAC
 TGCACACTTCTCAAGACAGCCCTCTACGACATTAATGCAATTAATTA
 TTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 ACACGACTCAATTTCCACGCGCTATTTCTTAATGATGATGATGATGAT
 TCAAGATATTTTGGCAATGAGAGCTCACACAGCTTCAGACAAAGAT
 CGTGTGTGTGAGAACAGATATTTATTCGATCATCAGAGATGATGATGAT
 CAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC
 ACTTGTATCT
 ATATCAAGTGTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 AGGCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 CTCTCCGTCACCAATTTTCTTTCACAAACCTCCGCAACAGACAG
 CACTGTGATTTGTATCAGATTTCTTTCAGAGGTCTCAGACAAACAG
 AACCAGGTCAACAAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TTTGAAGATTAATGGAATAACACCTCATCTGATGATGATGATGATGAT
 CTGCGCATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT
 TGAAGAAATAATTTGATGATGATGATGATGATGATGATGATGATGATGAT
 TATGCTTACACGCGCTTACAGATTTTACAGAGGCAAGAAAGATATTT
 TATGCTTACACGCGCTTACAGATTTTACAGAGGCAAGAAAGATATTT
 AACCAATGACACATCTCATAGGCTGGAATAATGCAACAAACCTTACA
 CAGCAATGACATGATGATGATGATGATGATGATGATGATGATGATGAT
 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 CAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 AACTTAATCTATCTCAATTTGATGATGATGATGATGATGATGATGATGAT
 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 TTTGGGTTGACAAAGATTTACTTTATACCAACACAAATTTGATGATGAT
 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 AGATGAGGCTTTTGAAGATGATGATGATGATGATGATGATGATGATGAT
 AACAGATTTCTTTTGAAGCAATCAGCAATTAATTAATTAATTAATTAAT
 AATCAAAAAAATTTGGAAGAAACCTTCAATTTCAATTTCAATTTCAAT
 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 TTGAATGCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT
 AAGAGCAAGTAACTCAAAAGATCAGCTTTTACTTTCTGATTTCCGAT
 CGAATCACAAGCAAGAAAGCTGATTTCTTAATCTTAATGGAATTTTA
 TTCAATTCACAGTAA

YOR372C, 554 aa (SEQ ID NO 372)

MBDISYQOYVTSGTANATTSRNPSTDNADTNFLKWSFKYNFNSPLP
 TTTQFPYVSSNYQOYQDFRANTDANSSNESSSTILPHHQOIQO
 QOOOQO
 SEPLVASPEQFKEFLDPSSTNFPFHKTPTAKTPLRATVDSNGAQOSTTE

44/251

NPQQQNVFNVN/LLNLLKSNKTPSSCTGAFSRTPLSKIDNMLMFNQP
LTPSPSRFSSLSLTPPYGRKILNDVCTPVAKALISNSALVDFQKARKOI
TTWATSIGLENNILQRPPLRSNNKKLFIKTPQDFTINSTLTOKONENK
QDIYGSPTTITQLNLSISIKSLDNSRIPPLASRSDNILDNSVDDQI.FD
LGLTRLPLSPNPNCSLHSTTGTSLQIPELPKMGSRFSDTGINPISSS
NTVSFKSGNNSKGRKIKQNGKPKPOIIVANIQFNQDTSSSSLSSS
LMASSSAGNSNVTKKRAKLRKSQSLSDSGSKSQARKSCNSKNGNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)
TTTCTTCAACACGACGAGTAACTATTGTGCTCTTTTGTGACCCACCA
AATFACACTCAATCCAAATGCTTCCAGACGAGGCGGAAATTTTGAAC
AGCGCTATGAATTTGTGTAGCTCGCGGAGTCTCAATTTTGAAGAAAC
GCGGTGGGTCTTAACTGTGTAGAGCTCAATGTGCCCGCAAGGGA
AGGCTGTCTACATTTTTCGGCGTGGACCCCTTTCTCCGGGAAATAA
GAGAAGCATGGATTTAAATCAAGAGAAATGGCCTTAGTAGTGCAATA
CTACCTTGGTGTATCTTGTAAACACATGATTTGATCATCTCAGATGCTCAG
TTTCTTGTATGATATATAACACATGATTTGATCATCTCAGATGCTCAG
TTTATAAGACGTTTCTCTTTCGGCATTTTCGATTTATTATTATAA
TTTATCTCTATATAGCAAGTCAAAACCAACAAATAAACCATACACATACA
ATGTCGTGTAAGCGCAAGAAAGACCTCCAAAGCCCGCAGCTGAATA
GAAACGCGCTTAAAGAGCTTCCACTTCCACTGATGTTGAAGAGAA
GCAAGCTAGAAGGAACATACACTCTTCTTACATTTTACAAGTTTGAAG
CAAACTCACCTCAGACTGTTTTCGCAAGTCCATGCTCTATCTTTGAA
CTTCTTGTGTAAGCATATCTTGAAGAAATCGCTACTGAAGCTTCTAAAT
TGGCTCGGTATACGAAGATATCTCTGCTAGAGAAATTCAAACC
GCTGTAGATGATCTTACAGAGTGAATGGCTAAGCATGCTGCTCTGA
AGGTACTAGAGCTTGTACCAAGTACTCTTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)
MSAKAEKPKAPAEKPKPAKKTSTSDGKKRKARKETVSSYTKVLK
QTHPDGTSQKSIINSFVNDIPERIANTEASKLAAYNKKSTISAREIQT
AVRLILPGLAKHAVSEGTRAVTKYSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)
ACCAACCACTTCTCTTGTCTCTCAATATCAAGAAAGAAAAA
CCACTGCTCAGATGTTATAGGAAGGGGTGTTAACTTATATACAGGTTCA
TCTACCACTCACCAGTCCATACAAACTTGAACCGTCTCGGTACCAGTCTT
AATCAAAATGTTCCCTATGCTTCCAGAGAATACTGCTCAATGCTTCAG
TTCCTGCCATTGAGACTGTCAATAGAAATTTCACTACCACAGAATATCC
TACAACGTCATACAAGATTTGTTATTTTGAAGGAACTTAAAGACACCAAACT
GGCTCCAACTACTTTCGAAGTCTGTAAGTAAATGTTTAAAGCTTGAACCC
CACCACAAAACCAAACTTACCAGAAATTTGAACCTTCAAGGCCCGAGAGCT
TTAAAGGCTTACCCGAGCAAAATAGAACTGCTCATGTTGCTTAAAGA
GTCTGAAGAGGGTGAAGAGCAATTTGAAGAGGATTTGGCTAGTTTGG
ATGATGCTGAGGAAACCAAGAAAGTCAATTTGAACCTTTTCAATAGATCTTC
CTTGTCAAGAAAAAACAACAGAACCAAGCTGAAACAGATCATATTAT
TTTGGCTTTCTCTCTCATCTTTTATATTCGAATCCAGTACACAAATGCA
AAAAGGCAAAATACACTAGCAGCTTTTGTGAATCAGCCACACAAATGCA
GAATTTTATTTTAAACAAATAACATTTGATAGATAGACAGCTCTTTAT
CTTCTCTATTACTACTATCTTTTATTTTCAATAACTATTACTTTCTAAGT
ATGACCTACCGCTCTCTTGTGTAATAATAA

YLR294C, 109aa (SEQ ID NO 282)
MLMKPKVKVIELFIASSLSKKKQTEPQAEQDHYFWLSSSHLFIPESSTIK
KKQNTLRLCNPQHPKMQNLFFKQIKQIQLYIDTSLISFLLLFFFYNNYFELS

45/251

MTVASLVNKK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTACATGTTATTACCTTCTCTTCTCACCGTGAATATTTGTGTGTC
ATACACACCGCTAAAAACCTTTTGCATCACTTATACCTACATTTCTATA
GAGCTATTTTGGAAACAGATGTAAACCTTTTCTTTTCTTTAGTTTGTGAGA
TTGTACTCTGTAAGAGTACGCTTTATTATTATTATTTTCAATTTTATCTTC
ATACCATGTAAATATAAAGCGCATATACTACTACGATCTTAGTACAGCTA
GAATTGCTGAGGCTTACAAATTTGCTTTATTATTATTATATATGACGATATA
CATATAGTGTACAGCAAAAAAAGAGGCGACTACTTGTATGGCTAGCGCC
CGCATCTCTCGGAAATTCGGCTTGGTGGGCGAGGTTTGAAGGCGCG
ATAGAAATATAAGATGATATTATTATTATTCATCCCATGAATAGTAGAATC
GATATAAGATTCTTAAACCAACAGATACAGAAAGCAAAACAATAATAATA
ATGGCTTAATAAGTTTAACTACAGAAATTTCCCAATCTTCCACTAA
ACTCTATGTTGGAGACATCCAAAGGTACGCTTTATPACCTGTATCCATTTT
ATGCTATTTTTGGGTAGCGCTCTGTACACCACTTCTATATACATTCCAAAT
GCTATTAGAGGTATCAAGCCCAAGAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSTKPLMWRHPRSRALYLPFYAIFAVAVVTPLLYIPN
AIRGIAKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATAGCTATGTTTTTTATAGATTATGACCTTCTTGTCCACAGTAAA
TGTGGCGGGAAGATGTTAGCTAGCCCGTGCACAGTGGGAAGAGACGGA
GGCGATTTGGGGTTTCACTCGGATTTGCGGGAAGAGGCGCTTACACCGTG
TTGACCCACCCCGCTCAGAGTAAATTTACACAAACAGTGGTGGTGCC
TATGTTGATATACGAGATAGTATGATTAAGCTGCTGATTTGGGTTAGAAAT
TTTGTAGGGTTTATGGATATGATATGATATGCTTGGCTTGGCTAGGTAGG
TAATCCAGACACCACTGGAATATATATAAGGAGAGAGTCTTGGCAGGTA
GATTTGTACTCTCTACCACTTCTTCTCTCTTTTATTATGTTAATG
TTTATTATAAGCACAGCAAAAGCTTAAATAAATCTAATAAGATTTCATT
ATAACATAACATTAAAGCACAAATTTTCAACACAAACAACTTCAAAAC
ATGACCAAGACTAGCAAAATGTCAGCTCCAGAAAGCAAGTCTTAACCCAAA
GTATTTTACCCATAAGCGCACTTTGGGGAGTCTCCCAACCCACGCTCAAGA
GAGAGGCTATGGGAAGGCAATTTGGGGAAGCTTCCGCGATGAGATTAAAT
GACTTAATCGATTCTGGCGAAATTAAGACAGTCTTCAACAAAGACCAAGAG
GGGCTCTAACTCCCAAAACAATTAAGAAAGGCTTTCTGATTTGCAACAAAT
ACCAATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKMTVHEAKSNPKYFTHNGFGEPSNHVKRGYKGNWKGPGDEIN
DLIDSGLKTVFNKTRGRSNNQNNRRLSDLQQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTCAATGCGCGCAATAGGAAGCGCAAAACAAATGATGTAATTCGTAGGA
AACATGCGAGCCCGGAGGTGAGCACTGACGTACTGACGCTGGCTTTT
GTAGAAAAGATGACCGCTTGCAGAGAGGTGGGGAATTTGAGGGGTCTT
CGTACCCCACTTAAATGGAAGAAATATGATGAAGAATATGATGATTAAC
TCTTGAAGGAGCGGGGTTCATCACTTTTACGGATTGGTGAACACA
GGGGCTCAGTTCGATCTGGTATTTAGGCTTCCAGCGTTGGTGGTATTC
AGTTAGCGGTATGGTATGCATGCTGTTGATGCTTGGTGGTATCATTC
GTTAGGTGAATGAGCAGTAGCGATATAGATATATTTAGTATTTTATAG
CGTCTTTTGGTGGGAGGAGGACAAACCTGCTCGTAAATATAAAG
GACTTTCGATATCGCAGATACCTAGAGTATAAATTTGATTTGAGCGGAG
ATGACAAACATATTTCAAGTTGGTAAAGGCTGCTACCAAGATCAAGTCAGC

48/251

EEAQLQ000AQLLQ00A0FQ000PLKQRTGNSISDKYSDLNLTLLATGT
GIDTFGNTGEARIFAQHTKTFGFINSGTGYKQVNTNEPKNNPFLSNQYTG
LPSTNIVPTQGYGFGNQPSQPTNSPQNPFGISVSQFQ000Q00Q00Q0
YMNFO00Q0PQYQNFQ00PQVQYQ00PQVQI00Q00000000000000
GYTPDQVSLIDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)
CAGTCTTCAGAAATGCAATGCAAGTGCAGCAGCAGCTAATTCGAAAAATCT
CCAGAAAGGCCAACCCAAATTTTTTTCAGGGAATAAATCTTTTATGAG
CCACTACTCTCTCGTAGAACAAATTTCCGGCCCTCGCTCTTCTTATGAG
TTCACTCTTTACATTTGCTTCTGCGATATATTTTCAGAGCAACAAGGA
AAAAATAGATGGCAAAAGTGCCTTTCAAGGAAAAATCCCAACCATCTT
TCGAGATCCCTGTACTTATTTGCGAATGAAAGATGAAGAGGAGGA
ATACAAATATATAGAAATGAAAGATGAAAGATGAAATAGACGCAATA
TATGCCAATACTTCAATGTTCGAATCTATTTCTTCAATTTGACGCTATTG
TAAATATATAAATACATCAAGAACCAACAAGCTCAACTTGTCTTTCTAAG
AACAAAGATTAACACAAAAACAAGTTTTTTTAAATTTAATCAAAA
ATGTCAAAAGACGCTGCTATTTGAGAGCAAACTCTCTGTGGACATCTCTC
TGCCTGTGACTAGCCTCCACTCGGTTTTATCTACACCATCAACAAGG
CTGAAGAGATGAATTAAGCTTATGTTGAAGGTAAGAGCAGCAACCT
GTGCTTGAATTTCCAAAGAGACAGCTCTGCTATGTACTGCTCTCTAT
TATGTGTATCATGATCGCTTTGCTGTTCTGTTCTGTTGCGTTGGGATCTG
GTACCATTTCTGTTGCTATCAATCAACCGATTTCTACAGAAATTTGGT
ATGAAGCATAAAGATGATCTATTTATTTGCTAAGGTTAGAACTGGTTT
GATGTCTCCATTTTCAACATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTT
CCAAATTTGGTGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT
GTCACTACATCATCGGATATTTATTTCAATTTGATCTATCAACAATG
GTACCAATATTTATCGGTAGAAATTTTTCGGTTTGGGTTGGTGGTA
TTGCGCTTTTATCTCTATTTGTTGTTCTGAAATATCCCAAGCATTTA
AGGGTACTTTAGTCTTCTGCTACCAATGATGATTTCTGCTGCTGCTGCT
CTTGGTTTACTTACCAACTTCGGTACTAAGAACTACTCCAATCTCTGTC
AATGGAGATGCTCATTTAGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGG
GGTGTATGACATTTGTTTCCAGAGTCTCCAGCTTATTTGGCTGAAGTGG
TAAGATCAAGAAAGCAAGCTTCTATTTGCGTTTCTTAACAAGGTTGCTG
TTGATGATCCATCTGTTTGGCTGAAGTCTGAGCTGCTTGGCTGGTGA
GAGCAGAGAAATAGCTGGTATGATCTCTGCGGTGAAATTTGTTAGTAG
CAAGACAAGGCTCTCAGGTTTGAATCATCTGGGTGAAATTTGTTAGTAG
TACAAATATGAGCTGATTAATTTCTTCTACTATGTTGTTGTTGTTGTTG
TTCAAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
ATGCTGCTGCTACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
ATGGTTGCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
AGACCAACCACTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GTTTCTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TTGTTTCTTCTGAACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TGTCTAGCTGCTCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
CATTTATTTCTGAACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CATTTATTTCTGTTGCTATTAATCTTCTTCTTCTTCTTCTTCTTCTTCT
GGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CATGGAAGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
GAGCTCAAGAAATGCTACCTACAGTACAGCCATTTGTACAAAGAAATGTT
CAGCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)
MSQDAATAEQTPVEHLSDVDSASHSVLSTPSNKAERDEIKAYGSEBEHP
VVEIPKRPASVYVTVSINCMITAFGGVFVGWDTGISGFINTQDIFRRFG

49/251

MKHGDTNLYSKVRTGLIVSIFNIGCAIGGIILSKLGDWYGRKVGILIVV
VTYIIIGIIQIASINKWQYFIGRIISGLVGGIAVLSPMLISEVSPKHL
RGLVSCYQLMITAGIFLGCTNFTGNTXNSVQWRVPLGLCFALWALFMI
GGMTVPESPRIYLAEGKIEEAKRSIAVSNKVAVDPPSVLAEVAVLAGV
EAEKLGNASWEGELSSKTKVLQRLIMGMIQSLQQLTGDNYFFYVGTI
PKAVGLSDSPETSIVLGINVFASTFVGIYVVERYGRRTCLLWGAASMTAC
MVVASVGVTRLWPNQDQPSRSGAGNCMIVFACFYFCFATTWAPIPVV
VYSETFLRVKSKMSIATAANWMLWFLGFFTFITGAINFYGYVFMG
CLVFMFFYVLLVVPETKGLTLEEVNTMWEGLVLPKWSASWVPPSRRGANY
DAEENTHDDKPLKRMFSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)
AAAAAATGTTTTTTTAGGCAACGGAGATTCGTTTTTATCCACGTTTACCCC
ACAAAATGTCAGGTACATTTGTCGGGCCCCGGCATCGAAAACAGTTTTT
TTCCTTTAAACGCTCGAAAAAAGAGAGAAATTAATGGAACCTTTGCGAGA
ATAGTCCTGAGCAATTCGAAATGTCTTAAAAAATTTCTGTTCTTAC
TCATGAGATTAATTCAGATGCCCTCGTGCTTCAATGAAAAAATCCAA
GAGATGCTCTCGATCTGTATGAGATTTTGGCTTGCAGACAAATGGAGAGC
AAATGGGTATACAAATATAGAAAGCACAGAAACATATAAAGAGCTCGAG
AAAAGACATATGTTTGTAACTATCTTCTTCTTTTTCCTTCTTCTTCTTCT
TTAATAATAAAAAAACAAGAACAAAGTTTTTTTAAATTTTAAATCAAAAA
AACAAAGATAAACAACAACAACAAGTTTTTTTAAATTTTAAATCAAAAA
ATGTCAAGAGAGCTGCTATTTGCGAGAGCAAACTCTCTGCGAGCATCTC
TGCCTGTGACTCGCTCCACTCGGTTTTTATCTACACCATCAACAAGG
GTCAAGAGATGAAATAAAGCTTATGTTGAAGTGAAGAGAGAGCAACCT
GTCTTGAATTTCAAGAGAGACAGCTTCTGCTTCTGCTGCTGCTGCTGCT
TATGTATATCATGATCGCTTTGCTGTTTCTGTTTCTGTTTCTGTTTCTG
GTACCAATTTCTGTTTCTATCAATCAACACCGATTTCTACAGAAATTTGGT
ATGAAGATAAAGATGATCAATTAATTTTCTTGAAGTTAGAACTGGTTT
GATTTCTCTCAATTTCAACATTTGTTGCTGCTGCTGCTGCTGCTGCTGCT
CCAAATTTGGGTATATGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GTCACTACATCATCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT
GTACCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
TTGCGGTTTTATCTCTATGTTGTTTCTGAAATTTCTGAAATTTCTGAAATTT
AGGGTACTTTTACTCTTCTGCTTCAATTTGATGATTAATCTGCTGCTGCTG
CTTGGGTTTACTTACCAACTTCGGTACTAAGAACTACTCCAATCTCTGCT
AATGGAGATTTCTTACCAACTTCGGTACTAAGAACTACTCCAATCTCTGCT
CTTGGGTTTACTTACCAACTTCGGTACTAAGAACTACTCCAATCTCTGCT
GGTGTATGACATTTGTTTCCAGAGTCTCCAGCTTATTTGGCTGAAGTGG
TAAGATCAAGAAAGCAAGCTTCTATTTGCGTTTCTTAACAAGGTTGCTG
TTGATGATCCATCTGTTTGGCTGAAGTCTGAGCTGCTTGGCTGGTGA
GAGCAGAGAAATAGCTGGTATGATCTCTGCGGTGAAATTTGTTAGTAG
CAAGACAAGGCTCTCAGGTTTGAATCATCTGGGTGAAATTTGTTAGTAG
TACAAATATGAGCTGATTAATTTCTTCTACTATGTTGTTGTTGTTGTTG
TTCAAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
ATGCTGCTGCTACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
ATGGTTGCTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
AGACCAACCACTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GTTTCTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TTGTTTCTTCTGAACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TGTCTAGCTGCTCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
CATTTATTTCTGAACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CATTTATTTCTGTTGCTATTAATCTTCTTCTTCTTCTTCTTCTTCTTCT
GGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CATGGAAGTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
GAGCTCAAGAAATGCTACCTACAGTACAGCCATTTGTACAAAGAAATGTT
CAGCACCAATAA

CAGCACCATAATTA

50/251

YDR343C, 570 aa (SEQ ID NO 122)

MSDDAALAEQPPVEHLISAVDSASHSLSTPSNKAERDEIKAYGESEHEP
VVELPKRPASAVYTVSIMCIATFAGGFVFGMDTGTISGFINQDTFLRRFG
MKHDGNTNYSKVRITGLVIFINIGCAIGIILSLGDMYGRKGLIVVV
VYIIGIIJIASINKWYQFPIGRITISGLVGIVAVLSPMLISEVSPKHL
RGTVVSCYQLMTTACIFLGTCYTNFGRKNYSNSYQMRVPLGLCFMALLPMI
GRTLVFPESPRLAEVGIIEAKRSIAVSNKIVAVDPSVLAIEVAULAGV
EAEKLAGNASWGELEFSSKTKVQRLIMGAMIOSILOLTDNYPFYRGTTI
FKAVGLSDSFERSIVLGIWVFASTFGLIVERXGRFTCLLMGASPTAC
MVVIVASVGTWRLMPNGDDQPSKSGAGNCMLVFACFYFCFATWAPLPYV
VVSFEPLRVKSKAMSIATAANMLMGFLIFPTPTPTGALNFYGYVFMG
CLVEHFFVVLIVPETKGLTLEEVNTWMEGVLPMKSAWVPPSRBGANY
DAEEMAHDKPLVKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCCTGGCATCCACTAAATATATGAGCCCGCTTTTAAAGC
TGGCATCCGAAAAAAGAAATCCACGACACAAATATGTCTTTCTCA
CCAACATCAGTTCATAGGTCCATCTCTTAGCCCACTACAGAGAACAG
GGCACAAACAGCAAAAAACGGGCAACACTCAATGAGTGAAGCAACAC
TGCCTGGAGTAATGATGACACAAGGCAATGACCCAGCATGATCTAT
CTCATTTTCTTACACTTCTTATTAACCTTCCTCTCTCTGATTTGGAAA
AGCTGAAAAAAGGTTGAACAGGTTCCCGAAATTAATCCCTTAATCTG
ACTAATAGATATTAAGACGGTAGATTAATGATGATTAAGTCTTTTATCT
ATTTCTTAACTCTTAAATCTACTTTTATTAAGTAAACATAAACAA
TTTAAAAACAAAGAACTTATGTTTGAATTAACACATTAAGTACATC
ATGTTAGAGTTGCTTAAACGGTTCCGTAATCGTAGATTTGATGTCTAT
GAGAAATTCCTTGTCTAGACCAACGTCGATGATTTGATTAAGTACATC
CATTTCTACCAACGACTACGCTGCTTACATGTTTGAAGTACATC
CAGGTAATGATACGCTGGTGAAGTTTCCACGATGACAAAGACATCAT
CATGCTGTAAGAAATGCTTACTTACCAAGAAAGAACACCAAGTAACTT
CATGGGTTCTTCCAGCTGCTCAAAAGACATTGACGCTGGTCCCAAGGT
AAGGAATAGACACTGCTCAAAAGACATTGACGCTGGTCCCAAGGT
TGTATATACGCTCCATCTCCACGCCCCCAATGTTCTGTCATGGGTGA
ACGAGAAAAATACATTTCTAATTGAAGATTGTTTCCAAACGCTTCTGT
ACCAACAACGTTTGGTCCATTTGGCCAAAGTTATCAAGATGCTTTCG
TATTTGAAGAGTTTGTATGACCATCTGTCACCTTTGACCTGCACTCAA
AGACTGTGAAGGTCATCCACCAAGGACTGAGAGGTGTGAACCGCT
TCCGCTACATCATCCATCTCCACCGGTGCTGCTAAGGCTGTCCGTTAA
GGCTTTCAGAAATTTGCAAGGTAGTTGACGCTGATGGCTTTCAGAGTCC
CAACCGTCGATGTCTCCGTGTGTTGACTGACTGTCAAGTTGAACAAGAA
AACACCTAGCATGAATCAAGAGGTGTTTAAGGCTGCGCTGAAGTTAA
GTTGAAGAGGTGTTTGGGTTTACACCGAAGACGCTGTTGTCTCTGACT
TCTGGGCTACTCATCTCTCCATCTTGATCTGATCTCCGTGTTATCCAA
TGTCTTCCAAAGTTGCTGCAAGTTGCTGCTGCTGATGACCAACGAATCGG
TTACTCTACACAGAGTTGCTGACTTGGTTGAACAAGTTCGCAAGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRALNFGRIIGRLVNRALISRNVEVVALNDPFIINDYAAMFKYDST
HGRVAGEVSHDKHITVDGKIATTYOERDPANLPMGSSNDIAIDSTGVF
KELDTAQOHIDAGAKKVVITAPBSTAPMFVGVNEEYKTSIDLKIVSNASC
TTNCLAPLAKVINDAFGLEGLMTTYSLSLATQKTVDGPRSHKMDRGKETA
SGNLIIPSTGAIAVGRVLELOGKLTGMAFRVPTVDVSVVDLTVKLAKKE
TTTDEIKRVKVAABGKLGVLGYTEDAVVSSDFLGGSHSSIFPAASGID
LSPKFKVLVSWVDNEYGYSTRVVDLVEHVAKA

51/251

YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)

CGACCCCTCTGTTAGATGACACGCCCGCCCACTGCGCAGAACTGTAA
CCCCATTAACCTATACCGGTACGAGTACTAAAAATGATATTAAGTAA
TGTATGTAAACAATTTACCGGTTTGTGTAAACATTCATTCATCTTT
TTGATCCCTTATGATCCCGCCGAGCATGATGTCAATTCCTCCATCTT
TTTGGCTGTATGATCCCGCCGAGCATGATGTCAATTCCTCCATCTT
ATCCGGGACTTCCGTCACAGTATCTTTTCTTCCAACTCCACAGATAT
GGAAAAATGAGGGCGGGGTATGAGTAAGCAGATGAGGAATTTGTAT
GAANAATGAGGTTCCGGGTTATATTAATGGGGGGGTTTCCGGTACA
ATTGATCTCATCTCTCTTCTTCAAAAATTTCTGGGTGTATGATAGAA
GTATCTGGAAAACCAACCAAAAACCTCAATAACAAAATTAATAAAG
ATCTTACGTAGACTAGCTAGCTGCTTAAAGCGTCTGATCTTCCATTGG
AGATCTCAATTAAGATATTTCTACACCTTCTCTAGAGTCCATCA
AGATGCCAAATGGGTGGAATATGACCAACACAGGGGTGTGTCAAC
AACAGTTTGTCTCTTAAACAGAACAGACCTTCGAAGCATTAACCC
TTCACGAGAGAAGAAATATGTATTAATTAAGAGTAGAGAGACGATG
TGGAGAGCGCGTGCAGGCGCCGACCGCTGCTCTTAATGGGCTTGG
AAGGTATCGACCTATTTGACAGGGGTAAAGGCTTTGTACAGTTAGCCGA
ATTATATGAACAGACAAAGATATGATTCCTTCAACGAGCTTGGATTA
ACGTTAAAGCTATCTCTCTCGAGAGGAGATTTGATTAATGATCATTA
TATTTGAATCTTCTGCTGCTGCTTCTTACACTAAGACAGCTTGGGTG
TGTACTGTAGTAACCCATTTTCTTACACTAAGACAGCTTGGGTG
TTTGTGGGCAATTAATCTTGAATTTTCCACTGTATTAATGAGGCTG
AAGATTCCTCTCTTGTGTACCGGTAAACCGTGTGTAAAGCTG
CGAATCCACCCCATTTGTCACCGGTAAACCGTGTGTAAAGCTG
GGAATTCACCTACCTGTGTGTATCAACATTTGATCCGGTTTGGTAAAT
CGGATATTCACCTGTGTGTATCAACATTTGATCCGGTTTGGTAAAT
GTGGGTAGGCGCATTAACCAACATTAACCAAAAGTGTGCTTAC
AGGCTTCAACGCTACGGGTGACATTTACCAATCCGACCGGACGCT
TGAAAAAATGACCTTGGAGTGGGTGATTAACCAACCAATTTGCTTC
CGGACCGCGAGTTGAAAAAAGCCCTGCAAAACATTAATCTGTATCTA
CTAATATCTGTGAGTCTGTGTGCGGTTCAAGCGGTGTATGTTGAAG
AATCTATTTACGACAAATTTGATTAAGAGTCAAAAGCGGTGTATGATC
ATCAAGGTGGCGACCATTCGATTAATCTTACTTCCAAAGTGCACAAAC
CTTCTAAATGCACTTAACAAAAATCTGAAATACGTTGATTAAGTACAA
ATGAAGGTGCTACTTGTATTAACCGGTGTGAAAGATTAAGTACAAAGGT
TACTTCATTAAGCCAACTGTGTGCGCTGTGTCTACTGTAAACCAATTAAT
TGTCAAAAGAAATCTTGTGCGCTGTGTCTGTCTGATTAAGCGGTGTGCT
CTGCCGAGGAATCAATTAACATGGCGAAGATTTCTGATTAAGCGGTGTGCT
GCTGTATTCACACCTTATATTAATTAATACCGCTTAATAAGGCTGTATG
AGTTAATGCGGGTACGCTGATTAACATTTATTAACGATTTCCACACG
CAGTTCTTGTGCGGTGTGATGATGATCTGTGTGCGGACGGAATATGCT
GTTATGCTTTTCAAAAACATTTCAAGTTAAAGCGGTGCTGTCACAAAT
GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MRSRTILCKTSASISGRLOLRYSFLPMTVPYIKLPNGLEVEQPTGLIN
NKFVPSKQNTKEVINPSTEEELCHIEGREDDVEAQAADRAFSNGSW
NGIDPDRGKALVRLAELIEQDDVLAISIEFLDNGKALISSRGVDVAVN
YKSSAGFADKIDGRMIDGRTHFSYTKRQPLVGGOILIPNFPILMMAM
KIALPALVGNVTVLKTAESTPLSLVYSKYLPAQIGPGLVINITVSGFKI
VGEATLNNPKIKVAFPGSTATGTHIYOSAAAGLKLVLLEGKSPNIYF
ADAEKKAUVONIILGIYNSGEVCCAGSRVVEESIYDKFIEEFAASIS
IKVGDPEDESTFQAGQTSQMLNKILKYVDIGKNGEATLITGGERLSGK
YFKPVTFGDKEDMRIVKEILFGPVTVTYFKSADVYINMAMDESYGLA
AGIHTNSINIALKVAIDVNACTWINTVNDPHHAFVFGGFNASGLGREWS
VDALQNTVLQKVAAPAKLDE

52/251

[illegible]

YER177W. 267 aa (SEO ID NO 152)

MSTRBDSVYLAKLAEQAERYEVENWKTVASSGOELSVPERNLLSVAY
KNVIGARRASVYSSITQGESSEKSHQVELYSKASKLETETLTKTSD
DILVSDHLPTPSATITQGESKVFYKMKGDQHYRLYAEFSSGDAREKATWAS
LEAYKTASEIATTELPTPHPTRLGLALNFSVYFYEIQNSPKACHLAKQA
PDDAAELDTYSESZYKOSTLIMQLLRNLTWTMSDMSGQAEQDQ000Q
0H00CQPPAAAGEGAPK

YOR267C, 2780 bp, CDS: 501-2780 (SEQ ID NO 363)

[illegible]

53/251

AAAACAAACCCACCTCCATGCGCGAAGATTCGAAAGGTTTTTTCAGACCTTCTCT
 TAAATATAAAACATATCTATGTCTCAACTTCGTGCCAAGAAACATAGCAC
 CATTTCCCCCCACCTTCAAAATCAACTTCACAGTAAATTAATATATCA
 CTATCGTCCGACAGCATCTCTATGCGTTTACAGAACCTCATGCTCATATCC
 AGTCGTGCTATACCCGCCAGTACCGATTCCTATCTTCTTTGTGTCCAATPAT
 ATTAATATATATATACAGATGATGTATCTTGCGTCAAAATACGGGAAAT
 GGGTAAGTTATTTGGGTTCCGGTGGCGGTCCGTTAAAGTCTTTGTGTA
 GACCAATGATGTGTGCTACTTTTGGCGTCAAGAAGATTCAGACAAGGAA
 CCGAATGAGAGTGTAAGAAGATATGCCAAGAAGTCCACCGCAGAAATTTTG
 TTTGGGTTGCACTTCAACCAATATCTTCCGAATTTGTGTGACGTGT
 TATCTGATCTTAAACAAATAATATCTATGAAGTTATGGAAGTACTGCTCG
 ATTGATNTTTTGTGTTGTTATAGACGGCAAGATGTCGTGCGCGAGAT
 CAACTGTTGCTTGAAGCAATTCACCTGAAGGTGTTAAATATTAATCTCTA
 TGGATTTGGCACAATAGAGAGATTTGAATTTGGAATTTGTGTCATGACTTCC
 CAGGSTATTTTGAAATTAATGATTTTGGTAGTCTGTGTCATGACATTA
 TCCTTTGAAGAATGCGTAAACGATGGTCTATGTGAATCTGGGTGATGACC
 CTTACTTAGCGCGGAAGTGATTAACCTCCACAAATCTTATGATCTCTCAG
 TCGCTGATATATGCTCTATTTTGGAGATATATATTTGTATGTGGCTTTAA
 AATGTTATCCGGAAGTATAGACAACGACTATGTTGAATTTGCCCAGGCAT
 CACGAAGAAGTTACTGAAAGAAAGAAAGAAAGCGTCAAGGTTTTTTGAA
 CTACAGTTCAGCTTCCGCCATTAATCAGCAAAATCAACAGCTCATGAACTAA
 ACTTGAAACAGTTTCCAAATCAAGTTTCCAAATCTCTCAGCATCTATACAG
 GGTAAACGGATACCAAAACAGACATTTGTGAAGAAGAAACCGAAGAA
 TAAAGAAGATGATAGCAATATGATATAAGAAAGCAGCCAGATTAATGACA
 AGGAAGTATCTGATTAATAATAGCAAAATAGAAATTAAGAAAGCAAG
 GTAGTTTCCAGCTTAACCCAAAGAGTAGTCCGATCGGACGCGCTGATG
 CGATGCTAATGGTGAATCTTAACGCGAGAGTGGATTTGCAAGGCTAACAGTG
 ACTGCAATAGCAAAACGGATTTAATGCTTAACATGACTGACGAGATCGAA
 TCGGCTGTAAAGTTGTTATCAACGTCAACACTGCTGCCAACGC
 TAACCCTGATATGTTGTTCCCAAAACATAGCAACACACAAACACATCAT
 AACAAACAAACAAACACAAACAAACAAACAAACAAACAAACATCAT
 CACCAAGATCAAAATCAAGACAGGCCCATAGTATGCTGTTCCGATATATA
 ATCAGATCAACAGCAAGGAGGACTACACATAAAATAATTTATCATAGGCC
 CATACCGTCTAATATGCTTACTACCAATGCTCAAGACCTTATCATGTCCC
 CGTATATCGCAAGTAGATATCCAAAGAAAGAAGCAACTTTAGATGATTTT
 TAAATGATGAATGTTTGTGGCGCATATGCTGCTGTACCATGATTTCAAAA
 ATAAAGTTTATAGAGCCTTGCCCATACATATGTTGGTTAGGGAGGAA
 AATGCTTACTTATAGAGACCTGACAGGTTTAA

YOR267C, 759 aa (SEQ ID NO 364)

MPNLLSRNPPFHGHNDHHDHRENSNPPQLRSKSFJLFI GRKQSNDS
LRSKSTDSMSKSTPTTPTTPTTNNNNHSHSNASTSTNNNNNYETNH
HNHSTSHGLHDYTSPTSPQTHSMGLKRFPRSNVKKLSMSQLRSKSHST
HSPPSKSTSTNNLNHVRQAHPHGFTHRYATQSAIPTSPSTDSISLNN
INIYHDDCI LAQYCKGLKLSGAGGSVKVLPRTDGTATFAVKEPRPRK
PNESVEYAKKATCEFGISTLHPNVJETVDVFSDKQNRKYVMEYCP
IDFAVNTVGMKSRSEINCLKQLTGKVGYSLHGLAKLDKNCVMTS
QGIKLLIDFGSAVFRYPEDGVTHAGHIGSDPLAPEVTSZTSDYQ
CVDIWSIGI IYCCW/LKRFPKA PRDSDDNRLXCMPPDI EHDVYESARH
HEELLKVERKEQRFLNHSDCSNNQQAHESNLTKVQNVNPTRPAISIQ
GSKDNKPDIVERTEENKEDDSNDKSTPDNDKESTDIKISLNENKST
VVSANPKVDADADCDANGDSNGRVDCKANSTDCNDIKCANVNDCSNE
SDCNKAVDTNNTANANPDV/PQNNPQQQQQQQQQQQQQQQQQQHHH
HQHQHQDKAHSIA SDKSSQHQRGHPHKKIITHGPVRLRLPHASRPTMS
RILQVDPKRRATLDI ENDEWFAITAACTCTHGPVRLRIPAHHTLVRE
RILQVDPKRRATLDI ENDEWFAITAACTCTHGPVRLRIPAHHTLVRE

NAHLETVKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)
 TATTTGGGCTGATTTCCGTTTGGGAAATCTTTGCGCGCGCCCTCTC
 AAAATCTCCGACAAAGTCCCAAGAAAGCGGGAAGAAATTAACGCGACCA
 AAAAATAAATAAAGCAATCTCGAAGCGGTGGTGAAGGCGCTCGA
 TTATCCCTACAAATTTTTCAGAGTAATAAACCCTTGTGTAAGTGGAA
 TTCCCATTTGCGGCGACCTACGCGGTATCTTTGCAACAACATCTATGCG
 GATACCTAGCAAAATTTTGCAATATGCTGCAATATGCGAATATGCG
 AGTCTTACTTCCACATTAACGCGAAGAAATGTGAATAATTTTGCAT
 CCTTGGCCCTCGTCAAGTAATAAGTGGCATGCTGTGAATATCTTCTCT
 TTCCATCCCTACATTTTCTAATTTCTTATCTTCTTCTTATCTTCTCTA
 ACATACCAAGAAATTAATCTCTGCTATCTGCTTAAACATATATCAATA
 ATGCAATTTTCTAATCTGCTTCTATCTGCGCGCTGCGCGCTGCGCTCC
 TGGCCCTGCTAAGTTACCACTGCTATCTGCAAGCAAGATCTACACTT
 TGGCTACCACTACTTCTTGTGAAGACCAAGTCTGTTGAACAGTCTCC
 CCAAGTTTGTGTTCCACCGCTACCGTACCGTGTGATGATGATTAATCTCA
 ATACACCACTGGTGGCCCATTTGACCACTGAAGCCCAAGAAAGGATCTT
 CTACGCTGCTCCAGTTACCTCTTACTGTAAGCTTCAAGAACACCACTCT
 GTGTGCTCACTACTCTGCTACCTCTTACACAGTGTGCTGCTGCTAAGGC
 TTTGCGACGCTGCTGCTTGTGTGGCTGTGTGCTGCTTGTGTGTGTGT
 AA

YLR110C, 133 aa (SEQ ID NO 276)

MOFSTVAISIAVAVAASAAANVTATVTSQSESTTLVTTSCEDHVCSEVTS
 PALVSTATVTVVDVITVYTWMCPLTEAPKNGTSPATVTSPEAPNMTTS
 AAPHSVTSTYGAATAKALPAAGALLAGAAALLL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGCTCTATTGTAATCAAGAAAGAACCTTAATCATTCGCGCTCCCTGTG
 TCGCTCTCGGAAAAACCGGTCTGACGCTACGTAAGAAATTCGCGACAT
 GGTATCGGACAGAAAAATTAATTCGACATGTAAGTAATTTCTTCTCC
 GTTAAGGTAGTGAAGCGGATTTTTCGATTTGTAATTAATTAATCACTTTT
 TCTGGCCAAAAAGGTCAATTTTGTGTGAATGAATGAATTAATTAATCACTTTT
 ATTCTTCTCTATCATTTCTTTTCTTTTCCACACCCCTCGGACGCT
 ATTCAATATTGTGAGAGTTAATGAATAAATAAGGCTGAAAAATTA
 AGACGAGATGTAAAGGAAAGCATTAACGAACATTAATTAAGAGCA
 CAATTTCTCTCCCTTCCATTTGCTATTAACGTTCTTTCTTTTAAGCA
 ATTCAACAACCAAGAACACACAGTACTACCAATTAACCAACAAC
 ATGCTCTCTTGTATTAACGAATAATCCAGCTGGGACACTACAATTTCA
 ATCAATTGCTATCAAGCCAAAGTATGTAAGTGAATCTGTGAATATGTC
 CACAAACAGTTGAATGTCTCAATTAATTTCTGAATAAGAAAGTTATC
 ATTACCGGTGCTCCAGCTCTTCTCCCAACCTGTACTGTACCCCAT
 TTTACGTTTACATCACTACTTGATTAATTAAGTGAAGAAAGGAAAGTTG
 ACCAAGTATGCTGTACTGTTGACACCCGTTGCTTAACCAAGCTGG
 GCTTAGAGCTTTAGTGTTAAGACACACACATCAAGTTTGGCTCGA
 CCCAGGCTGTGCTTACCAATTCATTTGTTTGAATTAAGCCGTGGTG
 ACGGTGTTTACTGAGTGTGATGGGCCATGTTTGTGAAGAAAGGATTC
 GTTACTTACGCTGCAAGAAACCAACCCAGTACGATGTGACCGTTTC
 CTCAGTCAAGAGTCTTGGCTCATTTTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLNKKFPADYKFOYIAISQSDASESCKMPQYEWMSKLISENKVI
 ITGAAPASPTCTVSHIPGIVINYLDELVEKEVDIVIVTVDNPNPANDAM
 AKSLGVKDTHTHIKIFASDPGCAFTKISIFELAVGDEVWISGRMANVVENGI
 VTYYAAKEINPGIDVTVSSVESVLAHL

YLR081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)

TTGTGCAACAATTTTGGGATGCTCTGCGCTGACGACCTGTATTTAC
 CTTCCTAGCTCATGCTTCCAGGCTCCAGCTTAATTTTTCATTTTCTT
 CTTCGCTGCGAAAGTTAGTGTGCGAATAATTTGTCATAAATTTTTCAC
 TAGATATTAAAGATATATACATGCAATTAAGATGCCAGACAGAGAT
 AGGCAATGAGTTAGTATGTAAGTACAGATATGCAATTAAGTGAAGCAAA
 GCGAGTGAAGAAAAAGAAATCCGTTTCCAGCTTCTTCTTCTTCCCA
 TTGCTTTTCTCGATCTTTTCTTCTGATGCTGCGACCTTGAACAAAGAG
 TACCTTCAATCTTGGCTTAATTTTGTATGATGCACTTTTGTGAATGAT
 ATTATTAATTTGTTACTATTAATTAATTAATTAATTTTGGTTTGGTTTGT
 AATTAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT
 ATGCAAGGCGAGATATACAGATCTGTTTGTGCGAAGACAGAGAT
 GGAATTAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
 GAAATTAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
 CCCCATTACATATCAATGAATAATTAACAACAGCTGATGCTTACAC
 CAACACCAATTAACAGAGTGAATTAACCAATTAACCAAGCTGCTTAC
 AATCCATTAAAGATCTATTTCCATTCGCGCGCTTACGAGGCTTACACAG
 AACAGGCTATATGACGCTACATTAATTAATTAATTAATTAATTAATTA
 ATTAAAGCTTAACATTAATTTGAAGCAAAATTAACAAAGCAATATCC
 ACTATATGCTCAATTCATATGTTACTGACATCTGAAAGCAACGTAACCT
 CAACTGTACTAATACAGTACATATGTTACTGACATCTGAAAGCAACGTA
 CAACATCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACCTT
 ACACCAAGAGGAGTCTCCAGGATCTTCACTTCACTTCACTTCACTTCC
 TCGTTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
 CTTCGATACATTTTGGCTTCACTTGGAGCTTCTTCACTTCACTTCACTT
 CGCTATCATCAACAACTATGTAACCAACCAACCAACCAACCAACCACTG
 ACATCGCGCGATTTATCAATGATTTACCGTGGGCGCCACGCTCCAGTTC
 GCTTATCTCGATCTTACATTTCTCCAGCAAGCTATGCTTATTTGGACCAAC
 GCCAACCTCTGCTATGCTCTTCCACACATCTGATCTTATTTGGACCAAC
 ATTAACCCACCGCAACATTCACATCCCACTGCAAGAGGAGATTTTTC
 GACAGCGACAGTGAAGTCTTCTGCTCGCATCACTTGAATGAATGATTT
 CTCTTTTGAAGTGGGCGTCAACACATGATCTTCTTCTTCTTCTTCTTCA
 CCAGCATCATCAAGACCTTTGGCATTTGGAATTAATGATGAGCGTTTG
 GAGTTGA

YLR081W, 368 aa (SEQ ID NO 30)

MPGQIISIFLQNEEDMDKYLEYSIKLLHQSSNSFOSHAPSHQSNYH
 PHVHMKYNTGTSYYNNNNNSVPHNQAGLQSTNRSIPAPYGAYNQ
 NRVADVPYMATYQKHHRSANNNNLNNQKXKQYPOYSNPVTTAHLKQYTP
 OLXNSNVNAHNNNNNNNNNNNNNNNNNNNNLNNYNOTFSTRYFNSNSP
 SLTSTSSNSSPYNGSTPEYLLPSTPAATNLSSSSNSNSMHTNPTTATS
 TSAIDLINDLPVPTSSLSLIDHSPTVFLPASQTLMSSTSSISGNT
 INPPOHSPSPQREDFSTPAVNMSASLLMDSLSLQWGSNHNWVSSSSQ
 PASRPFGIWNTDMSWVS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)

GTGCTGATATTGGGTTACTTGTAGTGCATTAATTCATCAATATTTAGCA
 GTCCTTCCAGGTGAACCATTCGCTGTGAACCATTAAGTAAGTAAGTAAGCA
 AGTGAATAATGTTATGATTTAATTAAGTACAGATTTGGAATAATTAATTA
 GCAAGTTTGGCTTATGATTAATTAATTAAGTACAGATTTGGAATAATTAATTA
 GTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 ACCGTGAACCAATGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 TGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
 AAAAAAGACTATGAAAAAATTAATTTGTTGAAGACAGGTTAGTAAATTTG
 TGCTTTGCTTGATCTTCAAGTTAAGAAAAATTTAATTAATTAATTAATTAATTA
 GAAACATCTTTTGAAGGTTAGAAAGATGATCTTAATTAATTAATTAATTAATTA

56/251

ATGCTTACAAATGGTAGTTCCTCCCTGGTATATATTTCTTTCTTCGTAGT
TTTTGTACAGATCACTTATACAGCTTTACACAGATTTTCCCGCTGTGT
GCACTTTTTTCCAGATTTAGAGAGGATGGTTGGTGACATATAA
AAACATAGGTTCCCAACCTATAAATATATATATATATATATATAT
ACTACATATATGCTTTCAGAAATATGCAATGTCAGATAATTTGTTGGGA
TTCCATTTGTTGATAAGAGCTATATATATATATATATATATATATAGAA
GTTCCTCAAGATTTAGGAATCCATAAAGGGAATCGCAATTCATCA
CAATCTATAAATATATATATATATATATATATATATATATATATATCA

YDR366C, 132 aa (SEQ ID NO 126)

MYTIGSSLVLFLEFVVVQITVTHLHRSLLCTFFSKIIIEBGCWVYK
KHFNLVYIVYVYVYLHICFEKYVNVIEIVGLPIIKAIILIGIONILE
VLLKDLGIHKRESAILHNSINIIILLYVYIH

YDR154C, 851 bp, CDS: 501-851 (SEQ ID NO 101)

TAGACGGGCTTCACGGCTTCCACTCATTTCTGTCTCTGTAATGGCGG
TGGCCCTTCTCACTTGGTGGGCTTAGCTGACAAAGTGTCTGTGGCAT
CCCTGTATAAATAAAGCTATTCTCTTGAGCCTTCTATCTTTTGGCCAC
TGTGTCATCATTTTCTCTCTTTTTCGCTAGATAGGTTATATTAAGAT
TTGCTTGAATTAATATCTCAACTCAATCCAACTCAACCGCTAATACT
ACCATGTCCCAATCTATTTGTATGTCGAGCTGATGCGCCACCAATGG
CCGTGTCTTTTCAAGTTGACAGCACTAGTCCCAAGACTGCAGAAA
ACTTCAGAGCTTATGACCGGTGAAAGGATTCGGCTACGCTGGCTCT
CCATTCCACAGAGTATTTCAGACTCTCATTTGCAAGGTGGTACTTCAC
TGCTGGTAAGCTGACGGCGGTAGTCTATCTACGGTGGCAAAATCCCAAG
ATGAAAACCTTCAAGAACACACACAGACAGACAGGTTGTGTCCATGGCC
AAGCGGTCCTCAACACACAGGTTCTCAATCTTCATCAACACCGCTTC
ATGCCATGTGTGAGCGGTGAGCATTTGTCTTTGTTGGAAGTTGTTGAGG
GTTACGACATCTTAAGAAGTTGAGTCTCTTGGGTTCTCTCCGGTGGC
ACCAAGGCTAGAAATTTGTGTGCAAGTCCGGTGAAATATATAACCGCTCG
CCTGGAACATACAGCAAAATTTGAAAGCACTATTCTCTCTTAATATAT
ATGTATATGATAAGGTATGTATGTATGACATCAATCTCTTATAACTA
A

YDR154C, 116 aa (SEQ ID NO 102)

MKTSRSTTDQCCPWPPTVQTPVLNSSPPFHAHGWTVSMLSLVKLLT
VTTSLRLSPWZLLPVPRLLELLPSPVNTNRSAMNNTAKIETNYSLLNY
MYMYKVCVCMINSYN

YHR162W, 890 bp, CDS: 501-890 (SEQ ID NO 213)

CGCTCGCTTCCNAGAGATTATCATATCTTCTCATATATTTCTCCATAC
TTAAGTGGGTAGCGAGGACCCCTCAATCTCCCGACCTCTCGCCAGGCG
GTACATCTTTTTCACAAAGCCAGGTGAGTACGTGAGTGTGACCTT
GGGGCTGCTATTGTTCTTACGAATTAATCTATTGTTTCTGCGCTTCC
TATTGCGGCATGATAGATGGAATAAAGAAAGAAAGAAAGAAAGCGT
TGAGTATATAATAAGAAAGAAAGAAAGTCCGAGAGAAAGAAAGACAAA
GGTTTTCTCGAGGAAACAGTAAAGTTGATACGCACATCTGTTGACAT
CGCTGACTCAATAGGAATTAAGATAGACGCGCAACCATTTAGTTCAATTC
CAGAAATATATAAGAGATTTATACAGAAAAGAGATTAAGAAAGAAAGAA
ATGTCATACATCTCGTAGCTTTTGTGATTTAGGGGTTCTGGCAAGTGA
GACAGGCCCCAAGAGGTGCTATTCTGGGCTCTTACTTTGAAATGGGCTC
TGGTTCTCGGATTCAGGATATGAGAGACCGGTGGGAAAAAATTTCT
GGTGTCAAAAATTTGCTGCTCTACTCTGCGCTGATTTGGGACCTGTG
GTCTTTGTCTATCAAGCCAAAGAAACATCTTTGTTGGCTTCTGTCACTGT
TTCTTTGTCTGACCGCTGGCTATCAATTTGGGTAGAAATGGCCAACTACAGG

57/251

ATACCGAATGGCGACTCTATATCCCAATTTGTGTAGCTATATTTCTCAGCGG
CCCGCAGAAAGCAAAAAGGAAATTAATCTACCGGCGAGATAA

YHR162W, 129 aa (SEQ ID NO 214)

MSTSSVRFAPFRFWQSETGPKTVHFWAPTLKWLVLVAFGSDMKRPVVEKIS
GAQNLSSLTALTWRTWSFVFKPNILLASVNSFLCLTAGYQLGRIANYR
IRNGDSISQLCSYILSGADESKKEITTGR

YGR243W, 941 bp, CDS: 501-941 (SEQ ID NO 189)

CCTCCACCAAGCAAAATGAACAAAGCCATCTGCGGAAAAATCTGAAA
AAAAAATGGTAGGAGTAAAGAAAGAAAGAAATAAAGGTTACCTCTGCAG
TTTGTAGTAGTCGGGTACATTTGCCCCCTTTTCTCTCTGATTTGATATTA
TTACCCCGANTACCCCTCATCTTGGGAGTCCCGCTTTTATTTCTCCCG
CCAAATCGGCTATTAAACGGCTTACGTCATCTCCGTGGCGGGTCAAGCGAG
CCGCTCCCTGGTTTGGTCACGCAAAACCGCAAGGCTCAACAAAACTAAG
GCCATCAT
TGGTGGGTTGCAATTTGGAGTATTTGGAGAAAAATTTCTTTCTCTCTCATTT
ACGGCGGAATACTTATATATAAATAAAGAAATACATCAGCTCTTTAAGA
CTATAGCATTAAGCAATTCAGACACATAGAAACACAAACCTATATTTTTTA
ATGTCAGCATCAGCTTTTAAATTTTGGCTTTAGAGATTTTGGAAATAGTA
AACAGGCCCTAAACAGTACACTTCTGGGCCCACTTTTGAAGTGGGGC
TGGTCTTCCAGGGCTAAATGATATTAAGAGGCTGTGTGAGAAAGTATCA
GGAGCACAAAATTTATCTTTTATAGCGACGCACTGATTTGGACGCTTG
GTCTGTTGTCTCATCAGCCCAAGAACTATCTGTAGCTTCCGCTCAATTTTT
TCTCGGTTGCACTGCAAGCTACCTCTCAACAGAAATGCTTAACCTTTTAGG
ATACGGAACGGTGAATCTTTTAAACAGGTTATTCATCAGATATATAAAGG
GGAGAACTCTGCAAGCGTGCAGCAAGCAAACTGCATCCACATCGATGA
ACAAAGGTGATCGGTACTAATCCGCCAATACGCACTGA

YGR243W, 146 aa (SEQ ID NO 190)

MSASAFNFAPFRFWQSETGPKTVHFWAPTLKWLVLVAFGLNDIKRPVEKYS
GAQNLSSLTALTWRTWSFVFKPNYLLASVNPFLGCTAGYHLTRIANPR
IRNGDSFKQVIHYIINKETPAVAALKQTASTSMNKGVTGTPNPPIITH

YBR050C, 1517 bp, CDS: 501-1517 (SEQ ID NO 43)

AAGTACGATATGTTAACTGTAACTATGAAGACTGAGGACTGAAGCTGAAGGA
CTGAAGGACTATAGTCAAGGGCCCAATGGGGAAGTCCCTTCCAGGCCAAT
TGCCCGATAGTTTGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
GGCGGGCAGCACTGGATAAAAACCGTGGGGGAGTCAATTAATTTATA
CGCTTATTTGTGTCAACACGGAACCTTATAGTTATCATTAATCAATCGC
AACAAAGCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TGAAGCTACTGTTATATATGCAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT
GTTCTCTCGAAACTTAGGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TAATATATTGGAATAGAAAAAATAAGAAAGAAAGAAAGAAAGAAAGAAAGAA
ATGACTTTGAGTAAATGCGACTCTTTTGGATTAATTTCTTCTTCTTCTTCTTCT
AGAGAAAGAAAGAAAGTAAATTTGTTGAGGGGCTGAGAACTTTGATGA
ATAGAAACGATATGGATATCTCTCCCGCCCTGCAAAATGTTAGCTATTGCT
TTAAAAAAAATCAAGTCTTTTGAATGCCCAACAGTGGAAATAAACAAGAA
AAGAATGTCATCTTCCAGCAATGAAGAAGAAAAATTTCCACTTCTCAGG
AGCAAGAAAGTTTAAATCTTTGAATTTAAATTTTAAATTTTAAATTTTAAATTT
ATCAATTTCTAGTAGTAAACAATTAACAATTAACAATTAACAATTAACAATTTGAG
AAGCTCGAAACCACTGTAAATAAATGAAATGTTTCTTCTTCTTCTTCTTCTTCT
ACAGAAAGTGGACATGATCAAGATTTGAGAACTTTTCTTCTTCTTCTTCTTCT
TGGTTTAAAGGCAAGCAAGGAGAGATATTAATGGGCAAGCCACGAGAGAG
GCATATCAAAATTTAACGATAACGTTGAACAGTGTATTTATACTGATGAGC

58/251

ATTTCATACAAAGGCTTCCTTCTACAGCGTGTGAATTCGACTGATGAAACAG
CGCCCTGTTCAAAGTCTGATGATCCCTGTATTTGGCAACGGAGCAG
TAAAGCAAGTTTCTATGATATTAACAGCGTTTACGTGCGAGTACCGAA
TTATTAAGCATGCGCGCTGCCACTGCCATTAATCAGTAATATAGTGGAC
TATACAGCGTGGGACAGATTTCCGATGTTCCAGAAATGTTTTTTTACA
GGCAGAGAAACAGATTTTCAGTACTGTGCTTCGGGTGATCCGATCTCA
AGTTATTCACATATGATCATATTCCTCCGTTAAACCTTCGTAACCTTCA
AGTCATTCGACCTTCAATTTTGGATGCGGAATGACATGATATGATATC
TACCGCTGAACAGAAATGATCATTCAGCTTACATAGACACAGATATAC
CCAACTGCTCTTATTA

YB050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLNLFQDPPEEESKFEVAVRTIAMPNDKCYPPAANGTYC
LKIISLNAQWKINKRMCMIPAVKKNFDFEQRSLINLMLWFILF
INCSKNNYNKNNKHSNNVTAKENVLPLQHKKVNNDQLENLFWRS
WFKARKRDINGKPREHIFKENDVEQCIITDEHFIQRLPSTRLNSTDEQ
RPSKSELDPCIGNAASKRSFYDINSVYASDAITTTAAATLISNSGD
YQRGHDVDRVPRNVLQAGETDFSSVLRYVSDLKLSNISHSPVKRSTIS
SHSTFIESETDVTDTDAETENDIDAYIDTSTPNLL

YE071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTGACGTCGATGATTAATCAGCTTCCAGCTTACCTTCCCTTCCG
AAGATCTACCCAAATGCTGAGACCTGTGATATACAGATATCTTTC
GTCCGACTGGCATTTGTTAAATTTCTAAGTCTTCTTATAGGAACA
TAAATTTGCAAGAACACAAATTTGCTCAATGATCAACAGAGGCG
GCATTTATGTTTTTCAATTTTTTTTTTTTTTGTGCGTGAATTAAGCGG
GATATTTGCCAAGTCATCTAAAGATGACCATTTTCAGACCTTATCTTC
GGAATAATTTTCCAGCGAGTGAACACCTTTCGCCAGTTGTGATCCGCA
AATCTAATCTACGCGGGAACGAAAGTGTGATATATATATATATATAT
CTCGTTATATATATGATGATGAGGAGAACAGGCTCCAAATGCTCCCAA
TATTTTATTTATTTGATGATGAGGCTTAAAGACAGCATATATATATAT
ATGACGGCGCACATCTCTGTGCTCAGTTAATCCGAGGCAATCCCTTAA
AGTCAAGAAACCCAAATTTCAAAGTTCGATCGAATGGAATTTGGCGT
ACTTGTGCTGATTTTGTCAATATGATGAATCTTAAACTCTCAAGTCCCA
GAAAGCTTGTCTCGTTTAAACAGAGCTGATGAAATAAATATAGAGCCA
GTCCATTTAATTTCTTCCCAAATCCCACTGATTAAGTCCAAAGATTA
TGAATATCTGTAAGATTAATAAAGTTGGCAGTATGACCAAGTGTATAC
ACCGACTGTGAGAGCTCTGTCCGCTATTGATGATGATTTGCTCTTTC
TCTAAGAAATATGAACAAGTCAAGATTTTGTATCTCAGTTACGGGACTT
TCAAGTGTACCGGGTGTGTTATGCGTANTGCGCATCATATTTTACAC
GACCATGACCATATCTTCCATGATGATCTGCTTCTAGAAACAACTGTCA
AGTGGCGGTGTAGTTTCAACAATATGACGGGTGTGAATCTTTTAAAGT
ATGGGCTCTACACGGTATGTTTGGGTGTGAAGTGTGTACCTTCCAAAC
GGTGAATTTATACGAATATTCATGCCCCTAAGGAAGACATATGCTTGA
TGCATGAAACAATTTATTCAGTGTGCAAGAGGATCTATCGGTGTGCTTA
CTGGTATTCATCAATTTGACAGCAAGCCAAAGCCCTGTGATCCGTTA
TTTTTGTGATTTGGAATTCGATACCTTCAAGAAATTAATTTGTCAAGGC
TAAAAATGGAATTAATCGAATTTTATCTGCTTTGATATCATGACCGTG
GCTCCATTTGATATGATGATTAATCTTGAAGGACTTGGCTTTTCCCTCG
GAGAACCAACACACTTTTATGTTCTTATTTGAAGCTCAGGGTCCAAATA
GAGACACGACGATGAGAACTGACTGCTTCTTCCAAAGATACACAGAT
CTTAAATTAATTTGAGAGGTATGATGCGTAAAGACCTGAAATTTTGTAT
AGACTTTGACCTTGAGAAATCTGTCCACAGACTGAAATTTCTTAAAGG
TGCTATACAGATATGATGATCTCACTTCAATTTGAAGATTTATATTCG
TATCTGCGGTGTGACGAGATTAACGACGCGGTTGATGATGATGAT
GCACCAAAACAGTTGTAAATCATGTGTTATGTCATGTCGTTACGCG

59/251

AAACATCCATTTTAAATATCGCGGTAAAGAGATTTTACGAAACAGATGAGG
ACTTATGTAACACATTTGTTTATGAAATATATTCATCAAGAAAGTGTCC
ATCAGCTGAGCATGGATTCGGTTTCCATTAAGAAAGTATGATACACTA
CACCAAGATGATATTTGAATATGATTTATGAAGATGCAAAAAATCACT
ACGATCCAAATGGAATCTTAAACCATACAGTACATTTGA

YE071W, 496 aa (SEQ ID NO 144)

MTAAHVAAQLTAEPYKRVKRNPNFKVDSEDLAFYSILSNDELINSQAP
EELASNQDMKKRYRQSNLILPNSDTKVSIMKYCNDKILAVPQGN
TDLVGASVPVDFEVLSTLNMNKKVRDPVSGFTKCDAGVVRDHOQLH
DHDHIFPLDLPSRNNQGVGVSTNAGLNFRLYSGLHGVLGVLEN
FGLISINILAKDNTGYDLQFLFAGETIGVTGVSILVAANKPRALNAV
PGIENFDTVQKLFVRAKSELSELSAFEFMDRGSIECTIEYLDKLPPL
ENQHNFFVLLETSGNNRHDDEKTLAPLKDITDSKLISEGMAKAKADPD
RLMTWRKSVPTACNSYGMKYDMSLQDKDLYSAATVTERLNAAGLIGD
APRPVVKSCGYGHVGDNIHLNIAVREPTKQIEDLLEFPVVEYIASKKGS
ISAHEGIGFHKKGKHLHTRSDIEIRFMDIKNHYDPNGILNPKYKI

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGGTAATCAACGGCCCTTCACAGAAACCGCGCAGAAATTTT
TCTGCTGTTTGTATTTTTTTTCTCTGATATCTCATCTTCTTTT
CTAATCTTTTTTTTGAATTTTTTTTGTGTACACTTCCACAAATATG
GATGTTTATGATCTCGAAGATATTAACCGTTTGTGAGATCGGTG
GTTCTTATGACACTTCTCTGTGCTAGACTCTCTTTTATATATTTTCA
TAGAATTAATAAACAAGATATCAACAACATCTTTTCTGTTCCGTTAAAA
TAATCTAATAATTAATAATGCAATTCCTACGATTAATCACTGATCTGTCACA
TTGCGCGCTTGTCCCGCCGCTTCAACATCTCTGAGAGCACCGTTTG
GAAGATCTACCATCTTGTGCTACATACATCTCTGAGAGCACCGTTTG
TTCTGAACAGTTTCCAGCTTGTGTTTCCATCTGATACCGTACCGTAA
ATGACGTTATCACTTAATTAACACACCTGCTGATTAATGCAACATGAA
GCACCAATAATACCATCTTCTCAGCTTCACTGAAAGCCAAACGTA
GCCAATGAAACCAACCACTTCTCAGCTTCACTGAAAGCCAAACGTA
CCTACACTGTGTCGCTGTGTAAGCTTGTGCACTGCACTTCTTAAATA
GCTGTGTCGCGCTTATGTTGTAATTTACTCAACCTTTTCTTAAATA
TATTTTGAATAAATGTTAATGATCTTCTTCCGTCATACAGCTTCCACAA
AATGCTTTATTTCAATTAATGATATTTCTGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSLNTPEGVHCQPLKHQRIPLDQIKSQPKSOLKSQPNKVLAKLLP
PTLVPLRLCOLPVLQMLVLPVCCMLNLFNIFLEKMLSTPFSIQLPQ
NPFISINKIWF

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAGAAATGATCAGGAGCGTTTCTTGCACACAGACAGACAGTAC
GGCAGCACAGCAGAAAGATGGAATTAACGTAAGCCCTCAAGACAC
GTGATATGCAAGAGCTTAAACGAGACAGATTAAGTCTTCTATGCTAAC
ACCAATATTAATTAATTAAGGAATATATAGTTATTAATTAATTCATAT
CATATCATATATCATATCATATCATATATGATATTTGACAGGCC
GCTTCTCCCTTTTGAATCACTACATATTAATGAGACCCCTTCACTTTGA
ATGGCTCAGTAAAGACCTTTCGACCGCTTAAGGGGTGCGGAATATCAT
TCCGGGTGATCTCGAGAAAGTGTATCTTATTAATTAAGGAAAGCCCT
TCTAGATTCCAATATTCAGGGTAACTCTTCAACACTGCGCAGAACATAT
TCCAATTTAAAGAAATAATTAATTAATTAAGAAACCAATTAACCAACAAG
ATGCTAGATCAATTAATTAATGAGAGATCTGAAATCTCTGCAAGATGAC
CACTACACCAAGGACATCATCTGCGCGCACGCTGCGCTGCGAATC
GGGACATATCATCAATAACATTAATTTCAATTAAGATTTCTACGCAATTAAG

60/251

TTTCTCCATGAGGAGTCCAGCAAGCCGGTTTCCTGTTTCTTATCAACAGGT
TTTTTCTTAGAGTGCTCCCATAGTGCACAGCTGTGTGACCAACGGGAGAAC
TGATATCAATACGGAAATAGACCGCTCTCAGGACATCTCAAATCTGTGAG
CAGGAAAAATCTTCTAGTGGTGAAGTGAAGACGCGGTCTCATCCACAGTT
CCCTTTACAATTTCTTCTGACATATAAAGGTTCCAGTTTGTTCCTGCCAG
CAACAGAAAAACAGATCCAGATATAGACCCCGAGTTATGGAATAAGGCG
ATCTCGAAAGATACGTCAGGACCTACTTTCTGTGAGCTACACAGAGT
TATTGATCTTAAGGTACTCCAGCTTTTCTTCCAAAGCTGGTCTGACTTAC
AAAAATTTGTTATCGCTTTCTTTCTCGGTACTCTTCACTCTCTCTGAA
GGCTTCCATACAAAAGTCTGTGAAGAGTCCGAGCCCATTAAGATCGAC
TGATACCTGGAAGTCAATTTGCTGAATGCACTACCAAGGACCAAGTG
TTAATGCCATATGCCAATAAAGACTTGGCCGTACATACCGATTTTACCA
TTTTTAGAAAAATGCCAGTTTCAGAGTTCTCAATCTCTACCTGTTTAC
AGAAGGGAAGATCCCATCTAGACCCATGAATTTACTTCTGTGAGCGCAT
TTTATGCTCCCGTAATGTAGAGATCCGATTTTGAAGCGTTATGAGGCT
TTACAAATTTGTCGTGTAATATATATATAGAAACGGGGATAGAGGTA
CTACAAATCCAAACCTTAATATCGAATCATCGACATATAACGAGCAATA
CTCTTCTGGGTAAATTAGAGGCTTGATTAATGCAATTAATCTCTCCCA
CCATACCAAGCACCTTTCTCACTTTCCGAATTTATGATAGCCCTCAGATCT
AAATATAATCTGGACTTGAATTTAATTTACACCACCGACCAATTAACAG
AGAGATTTTCTTAAAGTCTTTCTATTTGGGGTGTGAACCTTTGTTCGAGGT
CATATCAATGACTTCAACATCAATTTTAGATTGCAAGTTTGGCCGAAAACTG
TTGTGTTATTTTACACAGAGAAATTTTGCATGCTAACTCTTATTTACAA
GAGTCAACCCGAAATGGTTTAAAGGGTTCGTAATTTCCATGTGATTTCTTC
AAGCTAAATTTAAGTCTTGTGAAGAGAGTTTTCTCTCAATGCAAAATAA

YHL021C. 465 aa (SEQ ID NO 194)

MLRSNLGRSRIARLITTPRTTYSAAATAAANRGHIIKTVPNRDSSTIIT
 FPMSESSKPVUSCFNNVFLRDASHSAKLVTTCGLYHNEKLTAPQIQI¹SE
 DGKSLVKKWGDGHHQFLQPTFIDYKGSFSPVPAKQESRYRQPOLWNRK
 ILKONVALLSVSYNEFIDPKDSDKLTQTLVNLKFGFATISGT²VSSSSE
 GLTTQICERIGPTASTVHGHEGTFVNAASQVNAHYANKLPLHTDLP
 FLENVPGQILQSLPATGEDEDNTPRMVYFDAFATARNVRESDEFAEYA
 LQIVPVANYIYENGDKRYQSKPLIEHHDINEDNTLLGNVEALIKCIN³YSP
 PYADFTFGIDYKPSDLANNLDNLITTPAKLTERFLPKSFTRG⁴NLDES
 HINDFNNGFRQLPNC⁵CVIFNNRILHANS⁶LTSSNQ⁷MLKGCYFDS⁸TF
 KSKLFL⁹EEN¹⁰PHDK

YKL054C, 2717 bp, CDS: 501-2717 (SEQ ID NO 237)

[illegible]

61/251

[illegible]

YKL054C, 738 aa (SEO ID NO 238)

[illegible]

64/251

[illegible]

YOR121C, 101 aa (SEQ ID NO 356)

MFNLSTYNNHTRNTQKQLLEYFERRIPWYNPPFALFLRYVIDSEFKVLSR
QSKYFPVRFDSIGIHRFWQDNITSLDVPANNVSGNLNVI FLRPFKDNRL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTCATCATTTTTCGCTCAATTTCTTCCATTTGGGTTACCTTTTATTT
TGCCAGTTGGTCGTACTCGAGGTTTCTCCAGAAACCTTGCACCTTGAAATT
GTCCTCTTTTGGCCAACTAATATTCACAGGTGGTCAGGAAATATGTGCTC
GGCGATCGATCTGATCTATCTTCAATGTATTTACTTATCTTCCGATCATAT
TAAGCCGATTTTTCAGGCCGATTTTCAATTCATTTATTAATGTAGTGTGTGT
TAAAAATTTAAAGTCATATAACCTTTCTCATGATATGTATAGATATATGGG
AACACATTCGCAGAAAGTATAGAGCGGCCAAAATAATATGACGTGTAAAGA
AAGACGAAGACAGTTTGTAGCTTACAAAGTTTTCGAAAGAGGCTATGTGTAAC
CTTGATATATATGCACTCATATAACTTCTGAATATGCTCTATTATATCGTGAT
TTAATGACGGCTTGTGGCATTTCTGGCTCTTACAGAGGTATGTAGATTTGT
ATGCTGAATGTGCGCGACTACTCATCGAACCTTACAAAGTATGTAGATTTGT
CAATATTAATTAATCTCTAGAAATGGGTGAATTTCCAAATATATATTCCTC
GGATTCATCTCTGTGAATAAGGCTATAATATATAGGTATATACAGAACTGACTA
GAAGTCTCTCGTGAATATATAGGAATCCCAATATGTGAATTTTATTTCT
GTATACCAATATATAGATATATCTCTCATTTCCATTTCAATGTTTTCATTTAT
CCTATTACATTTATCGATCCTTTCAGTCTTCCCTTAACTCTCGGTGAC
AGCTTCTATAATAACTTATATGTCACCTATCTAAACACCGTATATGATAATATA
TTGTA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYRTIETHFPNINNSTKNWF^{EL}IG^{IP}SL^{IK}AILG^{IQ}NVL
EVLDDIGIP^{ES}IFLCTNIT^{IP}HSIS^{YV}SL^{SY}IIDPCISASSNFGD
SFYNNLCH^{YL}TPYMIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2: 947-1487 (SEQ ID NO 17)

CCGATGGGAACGTTCTCGGAAAAAGAGAATAATTTAAATTTACTTCTCAACTAAAAATCTCGA
GAAAAAAGCAAAATGACAGCTCTTAAGCGTTCCGTCGCTTTCTTTCTTAGAATATGTTCTGG
AAGTTTACAACAATCCACAGAAAGAAATGCGCTTGACATGATGAAGAACCATCATCCA
CACACGGCGACACAGTGCTTTATTTCTTTCTCTGAAATTTTCTTCCGCCATTTTAAATCA
CAAGGAAATTTTCTTCTTAGGGCTCAGAACTTCAGAGTGAAGAACGGCTTTTAGAAAAAC
AAGCAACAACGTAACAATTTGTGCGACACACCGAGCCTTTGAAGAAAAAATTTTTCACATGT
CGCTTCATAATAATATAGTTTAAAGTTATCATCCACATATATTTAGTTAGTTGTTCTTTTTTT
TTCTCTTAATCTTTATCTTTTAACTCATGCTTTCTACCTTTCCAGCATCGAAGAGTCCCA
ACCGAATATATACACAATAATGGCATCCACGATATCTCCAAGATGAACATTTTGAAC
AATTAAACCGCTTCTTTGGGTGACAAGTCATACATGTAAGGGGTATGTTCCGATTTAGTTTAT

65/251

CGTCTTATAGAGATCGTGTGTTTTCTTCTCTTTTTTTTTTTTTTTTTTTTTTTTTCTTATGCTTACATGTAAGAAGGGA
GTTACTTAATATGATGATCTTTTTCGCTTATGTAAGTAATTAATCTTTGGTC
CGTGTATTGATGGGAAGTAAGACCCCGAGATGAGTACAAAGAGATGTGGTTGACTTA
TCACAGTATTGACGATAGCAGACAGCAGAGTATCAATTACTTATCTGTTATTTTTTT
TTCTTTTTTTGTTCAAAAAGAGACAGAGTCTAAGAGATGCTATCAGAAGAAAAAGT
TCTCATTACTTAACAGCAAAATGTTTTCTCTTTTAAAAATGTAAGTCTGTTCTCTC
AAGCTAGCTCTCTCTCAAGGCCGATGAATTCAGACTTTTCCAGCTGCCCTCGTCGG
TCAACCACTGCTTTCTCAAGGCCGATGATGTCGATTTATCGGTTCCGACGATGAAGAAGCTG
CTGCCGAAGAACAAGAATGACGATGTCGATTTATCGGTTCCGACGATGAAGAAGCTG
ACGGTGAAGCTGAAGAAGTTGAGGCTGAAGATGATTCGCCGATCAACGCTAAGAAGGCTG
CTAAGACAGCTAAGCCAGCTGCTGATGATCCATGTCATCTAGATGTCAGCGCATGGGATG
ATGAACCAATTTGGAAGAAATGGTTTGTAAAGCTCAAGGCCATCGAATGGGCTTTGA
CTGTGGGTGCTACCAATTTGCCAATTTGGTTTCGGTATCAGAAGATGCAAAATTAAC
GTGTGTGTGCAATGCACAAGTTTCTCTTGGATGTTGTGCAACAAAGCTTTGAAGAAGACG
AAGACCAGCTCCAATCTACCGAATTTGCTGCTATGCAAAAATTTATAA

>YAL003W, 206 aa (SEQ ID NO 18)

MASTOFSK1ETUKLQNASLADSKYS1EGCTASQVADTVFKAFQSAFSPFSRWFNHTASKAD
 EFDSPPAASAAAAEEEDDDVDFGSDDEZADAEKKAERLTAAYNAKKAAPAKPAAK
 SIVTVLDPKPDDETLEEMVANVKAITEMEGLTWGAHQF1G1FG1K1Q1NCV1VZDDKVS
 LDD1QQ00STEEDDEHVQSTOIAANOKL

>YAL060W, 1649 bp; CDS: 501-1649 (SEQ ID NO 19)

AAAGACATGAGGAATCAATAAAGAGCGCTAAACGTGCGTCACACATAGTGTGATTGACGTA
TCACAGTTTCCTGTGTTAACTCCCGCGGTCTCTCTGTTTAACTAACTTTTCTTCTCTCATTA
GCATTCTCTGACAGCTGTTTATATACATCATATGTACATTATTTCTGATTCAGGCGG
AGCAGTTTAAACATCAAGCCGGATTGTGCTACGCTACTTTGACCCCTTTCGTTTCGACGG
AGAGAAGAAACCGGTGTTTCTCATCTCTGCCATTCTTTCTCTCTACGGGGTCTCTAGC
CTGTCTCTCTGATGATGATAATAGTGTGAACGTTAGAAAAGAAAAAATCGACATATAAAAGT
GGGGCAGATATCTCTGTGACAAATGCGCAATTTCAAGCCCTTTGGGCAGATGTTGCCCTTC
TTCTCTTAAAGAGCTGTAGTACGATTGACCAAGTCAGATAAAAAAATAAAGGAACCT
AAAAAAGTTTAAATTAATTATGAGAGCTTTTGGCATATTTTCAAGAAGGGTGATATTCAC
TCATATATGATATCCTTAGGCCAGAAATCCAAACCGACGATGAGGTTATATTCGACGTCT
CTTGGTGTGGGATTTGTGGCTCGGATCTTCAACAGCTGCTTTTACCTCTGGCAAATTCCTATGC
CTAAAGATGAGAGGCGCATAAATATCAACAGCTGCTTTTACCTCTGGCAAATTCCTATGC
AGATGTCAGGAAATGTTTTCACAGTTGGTCTTAAAGTGACAAGAGTGAAAGTTGGCGAC
ACGTGTGTTGTGATCTGCCACGATGTGTGCGAGCGTCGATTTGCTGGCCACACTCCAAAT
TTTTACAATCCAAACCATGTGATGCTGTGTCAGAGGGCAGTGAATAATCTATGTATCCACG
CCGGTTTGTAGGACTAGGTGTGTTGAGTGTGCGTGTGCTGTCGACAACTATGTATCCACG
AACATCACATTAATCCGGTTTCCAAAGGAAATCTCTAGATGTGCTGTTAGTGTCTCTC
CTTTCTTGTCTACCTGGCATGCTGTTTAAGATTTCTGGTTTCAAAAAGGACGTTTCAGCCT
TGGTTCTTGGTGTGCTCCATTTGGTGTGTACCAATTTTGGTATCTTAAAGGAAATGGGG
CTATGAAAATTTGTATGTCTGAAATTTGCAGAGAGACAAGATAGAAATGGGCCAAGAAATGG
GGGTTTGAGGTGTTCAATCCCTCCAGCACGGTCAATAATCTATAGAGATACATACGTTGT
TGACCAAGAGCCATAGGGTTTGTATACAGTTTATGATGCTTCTCGGTATTTCAAGTTACTTT
TGTAAACCTCTTGAAGCCATTAACAATTCAGGGGACGCTCTCCACAGAGAAATTTGAGT
GTCAAAACCTGTCTCCATTCCAACATGGAATGATCTCTCCACAGAGAAATTTATGACTG
GTTTCGATGCGCTATGTTGTCGAGCCCTTCGAAGAAGTTGTGTGTCCTCCATCCCAACGGAG
GATCGCCATGGAAGATTGTGAAGCAAACTACTCTGTGAAGCAAAAGGATTGAGGACGGTT
GGAAAGAGGATTTCCAGAGTTGTATGGATCAACAGGAATCCACGTTTAAGATTTCTATTGA
CGCTTAACAAATCACTGCGAAATGAAGTAA

>YAL060W, 382 aa (SEQ ID NO 20)

MRALVFKKGDIHFTNDIPRPRIQTDEVIDIWSWCGJGSDLHEVLDGPIFMPKDGEC
KLSNAALPLANGHEMSGTVSKVGPKVTYKVGDRHVVDAASSCADLHCWPHSKFVNSKPC
DACQRCSENLTAGFVCLGVTSGGFAEQWVSQHHIIPVPRKEIPDVAALVEPLSVTWH

66/251

AVKISGFKKSSALVLAGAPIGLCTIIVLKGGASKRIVSEIABERIEIMAKKUGVEVNP
SKHGHSIELRGLKSHDGEDYSDCSGIQVTFETSLKALTFKGTATMIWGPVPEF
QPMVDVIOEVMVMSIGVVEAFEEVVAIHNGDIAMEDCKQILTGKORIEDGEMGEPQE
LMDKESNVKILLTPNNHEMK

>YB1058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTCATATGTCGATTTGAACACTTTTCAGCAAACTACGCCAGCCGACGACAGAA
TTAACACACACAAAGAGATCTTCGAGTTCGATCTTTTAGCGACAGGGCATACACTAG
GTATATTGTATGGGATCATACAGGACATGTTGGAGTGGATGTTTCATCATTTCCAGG
AACTAAGCAACGTCCTGGAAAGCCGTCGCAACGAATTTGTAGTGAACAAACATGCTC
TGCTAATAGTGTATACCATATGATGTTTCATTAATATATCTCACTACTATATGTTT
GTTATTAAGAGAGCAGCAATGATGACACTTAAGTGAACACACATTTCACTCTCTT
ACCGCATTAAGACTCTTATGTTGGTGGAAATGCAATGCAATTAAGAAACCTGGTACACAC
TAATATGTTATGCTTATACATATTTGATTAATATATTAAGAAACCTGGTACACAC
AATTATCTCATTTATGATGATGCGGAAATACCTGATGAACCATCCAGAGTTCATGG
AATTATACCATATGTCGATTAACATAGCCGTCATATCTCTGAAATTTGAGATTTAA
CATTAAGCACTAAATCTTATATGCTTCTCAACGATGACAAAGATTAAGAGAGAG
AAGCATTTGGAACAGACAGACAGAGAAAGCCCTCAGCAAGAAAGCCCTTCCACCACT
CTTGCAATTAAGCCATTAATACGAGACAGCTGGTGGTATATGTCGCAAAACAGAGATCT
CACAAGTGAACACAGTACTTGAAGAAAGGATGCTTACCTCTCTGCAACCAACAAAG
GTATAGCCGCTCTGAGAGTGTATACACTCCAGGTTTATAGCTTTCCGATATGTGTA
GAGTTCACGCTGATGATGACGATGAATCAACGAAATATCTTCTGCTGGTGTGAA
CATCCGCTTGAAGGTTACAGATCTTCAATCTTAATTCATTAAGTGAAGTTCGCTG
AAAAACGGAAGGGGTGTCMAATGGGCGCTGAAGAGATTCCTGATGACGAAGAC
ATGAATGGGTGCAATAGTTTATCTGGAAGAGTTTATGATTAAGTACGATACCATGACG
CAGCAGATGAAGTCGTGAAGACAACTTCATCAAGTGGCGAGTCCGCTTATATGCT
CAGAGAAATGCAATTTTGAAGAGTTTTCATCAAGTGGCGAGTCCGCTTATATGCT
ATGATATCTCTGGGAAGTTTGTGACAGATGTTGAAGTTAATCAAGGAGAGCTCCATTA
ACTCTTAGATGTGCAATTTTGACAAAGATTTGAAGTTAATGATTAATTAATTAATGATG
AGCTTTAATAGCTCGACGAGAAACCTGGGAGGTTTTCAGGCCAGGCAAAAGATCTG
GATCTCTTATCCCGGGTGAATGTCATCCTGGGAGGTTTTCAGGCCAGGCAAAAGATCTG
CTCAGGAACAACCATTCGCGACATGAGCCAAACAAAGGCAACCTCCATCAATTA
GATACGCAAAATGGCAAAAGAAAGTTTTCGACTGCAATTCACAGTATGAATGAATTA
TGTATGAGCATGTGACATCAATGCAACATGACCATTCGAGAAATTTTACCTTGATTT
ATGCCCTTCTATCAACCAATTAAGCAACGATGACGACCAATTTGAAGAGCGCTGATCTC
TGAATCTCGTTGCTGCAAAAGATGGCATGA

>YB1058W, 423 aa (SEQ ID NO 24)

MAELPDETIQPMALTNVSHNIAVOYLSEFGDLNENLNSYASQTDQKDRREAHMNRQ
OEKALKEAFSTNSNKAINTHEVGLCRKPSGSGSNEYLKRKSGSPPTKSSRSGS
GANSRFFSFSMDVRGOADDDDEDDPNTFAGETSGLEVTDPSPNSLLKDLLEKARRG
OMGAEENGREDDEHMGANRFTGRRLSTIDADEVVEDNTSQRREKVTRELTFW
KEGQVADGPIRYDDPANSFYLSELNOGRAPLKLDVQFGVEVAVVYKKLDSYKAPT
RKLDGFSQGGRLGSPITPESSPAEVPKMETPAAEQPMPEDEPKQDTSIQIRANMKR
EVLHNSNDYVFLYEHTVSNMTDPSRNFTLVAFPIKPSINDETTLLKADLINSVVVQ
RMA

>YB039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCCAAAGTATACATCTTCTTCAAGTGTGCTATCAAAATACATACAAAGA
TAATTAATCTCTGTTTATATAGTATTTCTTCATCTTATGGTGAAGAGCGCACTGTTTATG
TACATTTTCTAGACGTCGGAACGTAAGCAATTTGTCATTAACAAACAAAAAGTAAGAA
GATATATGAATAGAGCTGTGCTGAACATAGTAACTATATCATGATGAGATTAACAAGGATG
AATTTTCGATATTTTATGAACGTTCTCATTTATTTGGAAGAAAGCTTTATACAGGATG
GAGAACCAATGAGCGCGGAGTAACTAGCGGAACCGGACCCGAAATACGATTAAGA
AGCGCGGAAGGAGGATCTTAATGATATCATCAGTTAAAGAAAGCAAAATTAAGAAC
TATTTGAGACTGAACCGTTTGTGTTAATTTCAAGTGAAGAAACAATGAAGACGAGCACTAA

67/251

CATATTTTATTTAGTATGATGTTTCACAGAAATTTGATCAACATACGACACGCTCCG
TAATGTGCCCAAGCCAGTAGTGGGTATCTTTTATAGACTTAACCAAGAGAACTTATG
CTACTTTGAAGAAATGCGAAATGCGTTTGAATATCATCAAAATATTTGAAAGATCAACA
AACTATGAAGATGTTGTCATCTACAGATGATGAATTAAGCTGAAAAAGCTAAATTTGG
CAAGAAGATGATGAAGCAGACGATGCTCTTAAAGATGATGTTGTCTATCACCTGATTA
ATGTGAGGCTACTGAAACAGTGTCTCTTAAAGATGATGTTGTCTATCACCTGATTA
AGGGTGTGTGTTCTTATCCACTCTCAATTTGGCTTAAAGCTGAGAAAGCATTTGAATG
ATCAACCAACCGCGATTAATGCTATTAATGATGATGATGATGATGATGATGATGATG
CCCATCTTACACATTTAATTTGCTATTAATGATGATGATGATGATGATGATGATGATG
AAGATCTGCTTGTATGCGGATTAAGTATTAAGTATGATGATGATGATGATGATGATG
AGATTTCCATTTTCTACAAATGACCCAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTT
CGATCTTAAGCCCAACATTAAGTGAACAAATCCCATCATTTGGGCAAAATTTGAGATGCA
CGAGCGCAAAAGTTTCCAGAGATTTGTAATATATCTTTGCTTACCAAAATTTGAGACAG
CAATGCGTCAAGTTTATGCTGCTGAATTTTCCGCAAGAAAGCATGATGATGATGATG
CCAGAAATGCGGCTGATTAATGATCAATCGTTATCTTCTTCTTCTTCTTCTTCTTCTTCT
CTGTCATTAATTAATGAACGTTGATTAATTTATCTGTCCTCTTCTTCTTCTTCTTCTTCT

>YB039W, 311 aa (SEQ ID NO 42)

MLSRVSNNAATSWMOHQAQVGLYKTNIPVTYATLKEVEMLKSIKNIETKTMKIVA
STRLSVAERAKLSAKTMDABQLFYKNAETKNI DVEATENGA PRELVAITSDKGLCGSI
HSQLAKEVRHINDONADIVITGDKIKMQLTHTPNNTIKLSINGIGDAPFPOGSAALJA
DKLSVMAKGTTPKISIFPNDPVSSLSFSESEKPIFNAKLTQESFSEKFEIDTDANVR
DLFEVTLANQMLPMAQGYAEISARRNADNASKMAGDMINRSILVNRHQAVLTNEL
VDIITGASSLSG

>YB062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGGACCAATGCTCTTACCCGAAATTAATGATGATATATACTCTTCTGTTTC
TAGATAATGCGTTATTTTGTGTCATTAAGTTGTCATAAATTTGTGGCGGCTTTTGTGCA
CCGAGAGCGCTCATCTGTTATATATACAGATTTTGCACATCTTAACTGAATGAAGAT
AATGAAAGATATATTCATCAACATATATCAACAAACAAATATGCTCATATATGAAGT
ATGTAATGATATATTAATGAAGTAAATTTCCCAAGCAATTAATCAATCAATTAATTAAT
TGCATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AGTGAAGGAACTTCAACAG
TATTTCAAACTTTGGTATCACACAGTGTGTAGGTTGATGATGATGATGATGATGATGATG
TTTTGATGATTTATATGCAAAATGCTTCCAGAAATCATTAAGAGAAATGATGATGATG
TGATTAAGGCAAGAGTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATG
ATGAGTACCCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
TGTCTGTCTGCTATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG
ACGATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ACGGTTAA

>YB062C, 115 aa (SEQ ID NO 46)

MLPESIOEWMIOEMDKGSAGCPDTFAASLPIRINKKTKATNDSCICTNYLEDEYPLV
ELPHCHHFTDLECSWLSRSTTCPICRDVNMGRHRIINEIDTTAELEEDWGMVY

>YB101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAATATTTATCCAGGGTCCATTAATGATGATGATGATGATGATGATGATG
AAGCGCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AAAAATTCGCTTGAACAAAGATACAGAAAAATTAACCTCATCTTCAATTAATATATG
TAGGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
GTAAGCTTTTCACTACTGTGTGTGCAAGTTGGGCGCTTAAAGGTTTATGAGGATGATG
TCGTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AAGAGAGGCGATTCGCGCTGACAGAAATTTGCTTATTAATTAATTAATTAATTAATTA
AAAAAGCACTCATGCTGATGAGAAAGCAATTAACCTTCAACGAAAGATGATTAATTA
AAAAAACAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA

68/251

GGGACAAAGAAGCTATGGCTTAGGGCCGCCAACCTGATCTCTAAATGGCTACAGCAGTTAT
ATCGGTGGTGGTCTTACAGATCCAACTCTTAATGAAGAAATCCATGCGTGTATATATGA
TCCGTGGTGGTCTTATAGAACAAACAACCTGGTGGCATTTGACAACTTTGATATGTTGATG
AGAACTTAGATATATGCTTAATTAATATCGAAATTTTAAATACGTGGAGGCCATTTGGTGAAT
TTCTGTTCTAGACGAAGGATGAAGAACTTACGTGCTGCTCTTATCCATTTATTTGGAACGG
CTGTGCAAAACAATCTGGATTTGGCAAAATAATTTATGAAATAGCAGAACTGGTCTGCGCAA
GCCCTTCGAAATATGCTTAGTGCAGAACAAACCCATCGATCGACAAATCAAAAGCTTTT
ACGCATCTCTAATCTTAATGAAGAACCAAAAGATATCTTCAGAAAGTTTTCCTCAAAATTA
ATGGGCTGCACTAGACCTGTATTAAGTGATTAACACGCCCAACCAAACTGAAAA
TACAGGCCATTCGCTTATTCAGCCCATATTTGTTCATCTGTGTTAAGTTCAGTGAATAATATA
TCACTGTGTGACAAAGGATGGAGATTTAAAGATTCAGATTGGTGGCTGTCTGACAGTA
TTAACTTTGAACATCATAGATAGATGTCGTCTTTCTCTCTCACCTCATATCTTCGCGGA
TTAAATTTTAAAGAACGGAATTCGACAAATTTGAACGAAGGTTTACAAATCTTCGAGCCTC
TTAAGACAGACATTAATGATAGACGATTTATTTAGCCGTAAAGATGATATATGA

>YBR101C. 290 aa (SEQ ID NO 50)

MEKLLQWSTANSOGDKEAMARAGQDPDKLQQLFGGGPDPPTLMKESMAVIMPEVDE
TKLVAFDNFEMLTENLDNANNIENKLWEPLDLVLVQTKDEELRAALSIITGTAQNNLID
SQNNWYDNGLSLAISADSKTLPDLVBTKAFYALSNIRHNDIISGKPFKJAGLDCIA
PVLDMNTAKPLKWRALJALTAIYLSVKYDNIENISVLKOGVITESTIECLSDENLITID
RVLSFLSHLISSGIKFNEOBLHKNEGYKIEPLKORLNEDDYLVAKVY

>YBR139W, 207 bp, CDS: 501-207 (SEQ ID NO 55)

GGAGGAGTCAAGGGCCTGGAAAGATACGGATCTCTGTAGAAATATCATCTGGCAATATTAATCTAGT
AGTTTATTTGTTGGTGTCTATTTATCATATTTGAGCTGTGTATTTGACGCAAAAGCAGAGGATAAT
GAGTTTGTCTCTACTGACTCCACGCTAGCTGGATTTGGATCTTTTCTCCATCTCTTTTAA
TTTTTAACCTTTATTTAGTGGTTGGATCTACGTTTCTTTGGAGACTATTTCCAACTCTGTGACTATTG
TTGGATAAATACGTTTGTGACTCTGTTTAGTATAATCTTTTCTTTTCTAAAGTGCTTTAGAGTT
CTCTAAGATGTTCTTCTGTACAATGTAGCGCATTTAGGAAATTTCTCTAAAATATGGCCGGGA
GCGCAGCTAGCATCTTACGAAAGCTGAGATACAGCTTTAGGAAATTTCTCTAAAATATGGCCGGGA
CAGGGGTATATATAGAACGAAATATGTATCTCTGCAATTTTCTTTTAAAACAGCTCTATGACA
AAAAGTACATACCGACATCAATGAAGTATCTTAAACTTAGTTTGTGCTCTCAGCTCTCTCTT
TTAGCATCAATACGCTCATCTTCGGCGAGCCCTTTTCTCTTTTGAAGATGATATACCACT
TTTGCANATTTGGATTAACAGCTAAAGCTTACGCTTCTTAACTAGGAATACACAGCAACCCCTTAAATTTGG
ACGTTTGGAACTCACAGATGATCCGCTGTTTACAACTTTTATTTCTCTGTGGACACAGATTT
ACATTTTGAGACTTAGAACATAGATCTTCTTAACTAGGAATACACACCGCTTAAACCAAT
GTTGCGGTGTACATGACATATAAGATTTCCAACACTTTTGTGTTTACTGGTGTGTTTGAAGATTA
GGAAACGATCTGCTTAAACGACCCAAATATTTCTTTGGTGTAAATGGTGGAGCTGTGTTTGTCT
CTTATCACTGGGTGTCTATTTGAATAGTGGCCCTCATCAATTTCTTGGTGTGTTTGTGTTTGTCT
TCCAAATCTCCTATTTCTTGGATATAAAGCGTCTCAATGANTCTTTTAGAAACAGCCGACATCG
GAGTCGGTGTCTCTATTTGGATATAAAGCGTCTCAATGANTCTTTTAGAAACAGCCGACATCG
CGTACATTTTCTCGGAATTTGTTTTTTTGAAGCTTTTCTCTATTTAGCCTCCAAAGATTTCC
ACATATGACGGCGAATCTTATGACGAGCAATATATCTCCCTCAATTTGCACATAGACATGATAG
TCAAGAACTCTGTAAGAAGACGTTATATTAATTTACTGATTTGATTTGGTATGTTGATATCATG
ACCTTTCCTTCAAGCAGATATATTTGAACCAATTTGGCAATGGCAATGGGAAAGGGGCTATCCAC
CTGTTCTCTCATACAGAAATGTTGAGAAATAGTATAAGCTCAGCTCTGTTTGTGTTGTTAGGT
TGAACAGTTATGTTTATGCTTTTAAATTAAGTTTACATGCAATGTCGACACTGCTTTACT
GTGACTCTGCACTTTTGGAAACCGTACATATAACACAGGATCAACGCTCTATGACATAGAG
GGCCCTGTGAAGATAATAGTACTGTATGGTATGTGTATACAGTCTCTCCGCTATGCTGAC
AGTATATGAATTTTCTGTAAGTTTCAAGAAACGCTTAGGGTCCGACGTGCATATAATATCTCTG
GCTGTGATAATAGCTGTCTACCGGATTTTGTTTTGAAGCGGATAGGAATGAACCAATTTATCTG
AAACATATATTTGCTGAAATTTTAAATACAAATATCTCCGTTATTAATATGATCGGGTGTATA
AGGATTAATATTTGTAAATTTGGCTGGGAAACCAATGCTTGTGCTCCAAATGAGTTGGAAATGGAATCA
ATTAACCGTAGGTTATCAGAGAGGATTTTAGAACCATAGGGTCAGTAAAGAAACAGGTTGAAG
ATTTGGGACAGTCAAGACTATGGCCCTTTACCTTTTGTGTAATATAGGATGGCCGGTCT
ATATGGTCCCTATGTAACACCGGAGCAAGTTTGGAAATTTGGTAAGTCAACAGTGAATTTCCG

69/251

GTAATCGTGCTTTTTCGGATCTTTCCACCTTGGAAAAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLFVLQLLISIKYASGRFSLFEDDTTFANLDKQLPQNTQTLKLDRLNHDH
 PLITTFISSVDVDSYLRURTVDPSKLGIDTVQWGSYMDYKDSKHFYWFPEPSRNDPAND
 PIIILWNLGKGSSTYGLFELGSPSSIGADMARPHNPYSWNNNAISFLBQLGVLGVSFGY
 DEKVSZLKKAGGADYI FLELFPSPHLSRNDPHLITAGESYAGHYI PQIAHEIYVNNPRT
 PNL'YSMTNGITDPLIQADYYEPMACGGGYHVLSSSECKMSKAAGRCRLNKLCA
 SKSSLPCIVATAYCDSALLEPYINTGLAVYDTRGPCEDNSTGCMYTLGRVYDQVMPNPE
 VQHTLSGDVHNYSGCNDNDVFTGLFTGDSKFPQYVIAELLAHNIIPVLIYAGDKDYICNW
 LGNHAWSNELHINKRYYQRRMLRPSKSTGEELGQVKNYGPPTFLRIYDAGHWPVYDQ
 PEASLEWMSNIGSRRFSDJSTLEWAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TCGCACATGTTGAGTATGCGTATGCGCATTTTCCCTATTTCTGAGRAGGAGTATGAAAATAAT
TCCCGAGGGTTCAAGATGCTCTTTTGTAGAAATAAATAAGATGTAAATAGTTGGAAATGTAAT
CTTTAGTAGACAAAAGAGGTAAAGTCTTTAGTGGCCCTTTGCGGATTTAAACAGTATGCTCTTT
AGTGCAAAACACAGAAATGAGCTCCCAATCTTTGTGACACAAATCGACACCAGGAGGAACAATA
CACGTAGAAGGGGATACTAAACACTTTGTCTGTGACAGAGATTTTGGAGGACACACTAACAG
CAGAACTTTGCCCTTCTTAACTCTCTGTTTATGATTTGCTTGAAGTATTTACACATGTATATAAA
AGATGATATATTTTTTTTTTTCCTCTAAAAAAGTTCTTTCTTTGGAAGTACCCCTGTATAAAA
AAGATCAATAATGGAACCGTATCATATATCAATTTCCGGGAGGAGAAATAAACGCAAGACC
TGTGCGTTTCTAGCTAGTATGTTGACAGACAGATAGAGTGACTCTACATCTACAAATGCC
CTGAGATATCGGTATATCATATATGCCCAAAATGACATCTATTTGACTCTCTCGTGGAGGTT
TTACGTGTGTTTATCAACAAGGTTGGCTATTTAGAGGAGACTTGGAAAGCTTTGGATTAATCTCT
TTACAGAGATCACTTGGAGGCCGAGCGGCACTTTGGCTAGAAGTTTAAGCGTTTATAGAAA
ATGAATCTAGTGTCTGGCTTTCTAGTTTCTCAAAATTTCTGGGATGTGCCGGGAAGTTTAA
TTACTTAAACCGAGTCTCAATTCATTTACAGTGAAGAGTTTGACATGAGCAGTACTTTC
CTCCGAGAGTAGATTTGAATCTGTCTATCGAATCCAGAGAATTTTACATATGATATATCAG
TGGAGCCCAACAAATCCAAATGTTGTGAATATCTGTCTGTTTGAACACGGGTGAAGAATTTA
CAATTTGCAAGAGTGAAGATGAGAACTCGAAGTAGGTGTATTTCTTTGGTGAATGCAAGTG
ATGAAAGTGATGTGATATTTGGTGGAAATCACTTTATTTGATATAACACAGGCCATATCGCATACAATCACT
TGGAAAGATGTTCAGAAAACATCTTTATTTGATATAACACAGGCCATATCGCATACAATCACT
CGACACTACGACATCATCTGATATGTAATGAACCTATCCGTTTGCATCTCNAAAATCATGA
TGTGATCTCAGATTTCCGAGAAGCCCTCAATGCAATGTATCTTAATGACACCTTGCAATGCG
CGTTAGAATATTTATTCGATATAATTTCAATCTCTCTCTTACTTACTTTTGGAGGAAGACG
ACTTTAGAATTACAGAACTCTCTCTTCGAGATAAGGCAATGGGGTTCGAAAATATCTTTTG
ATATTAAGGGGCACATGAAATGAAGTGACATGCAATAGATATATTTGAGCCCTCTTA
AATTAAGAGGGAATAATTTAGAAGTTTCAATTTGATTCAGAAAAGCTCTAGGATATGATATCTC
CAGGTGACAAATAAAGTTTCCGTAATCACTTTATTAATAAAGCTCTAGGATATGATATCTC
TCTTTACAGACGATACATCTCCCGCATTTGAACTCGACAACTCTTCTAGTACCAATTC
CAAGGCCCTGACACAAGGATATTTCCAAAGATCAAAAAATGGTAGCTTACTATGCTTACTCA
TCTCCAATCATATACATTTTCTCAAGGTATTTGGTAAACAAAGAGAAGAAATCATGATA
AAGCGGGAATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MYTRHRVTVLYNAPEDIGNHMQNDTHLTVRGSGVVLOQRWLLERTGSLDKSFRITWTR
PRADRLSIVTENSIESAGFVYSNSDVPERFITNPVNSPHSEKFDIEQYLPPEVDLN
LSWNPEDFTQIVSPTQIQIYEYRLLKQGEFTIARVDEKLEGVFVDADESQSDVI
GGICRNWRMDGKMERCKQTSLLYKQGHYAYNHSTFTTSLYNEPTLGHFKMTD
ERPKMTYLMHQLQIPLUEFLDKFQSSPLFGEDDLEPEVSLRDKAWGSGESIPELKACTM
NEVTLTHTRYIPEPSNNKDKLEVSFDPEVTLTCLDCTGNYISRPFFYKGLGYESLVTDDTT
FRLHNSSTLLVPIDPRDTPKQSKINGKTLGTLQYIVTSKVFYGNKKRSVKRE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAATGATTACGAAATATAGATGATGTAAGCAAGGTACGGTTATAAACAGTTAA

72/251

CGAAACCACTGATCTCTCAGCCCTCTCAGCTAGCCAAACAGCAGCAGCAACCTCCACAGGATA
TTCTTCTAAACTCTATCTCTCTGCGCAAGAGTGTTCGAGATATGGTAG

>YDR073w, 169 aa (SEQ ID NO 92)

MSSEIAYSNVTNTNENRNTVGTVDVNTNANANANANATANATANATAEINLPTVDE
QRQYKQLLLHNSILLARVIQNNNSIQNNLNQNNINNNNNIIRIQQLISQFLKRVHAN
LQCSIQNGVPSAKPILITPPQLANQQPPQDLSKLYLLARVFEIWL

>YDR178w, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGCGGTCAAGTCTCTAGACCCCATGACAACAACAGCAGCCGCTATCATCGA
GGAATTGTGAAGTGAATAGATCAAAAAAAGCCACCAAGTAGTAATAATAAAGAA
TAAATAAACAATATAGTATAAACACCAAGCGAGGATGTTTCATTGTGCACTCGTGTCTT
GATGATCAATCAATCAATGTAAGAATTAATCGGCACGTTAAATGTTTATTAGAAATATA
AACACTTTATGTGCCATAAGCATGAGCAATCGCTGCTGTTTTTTTATTCCGGGGCAC
CTTCGGAAGAACACAGCGGCAATTATGATATAGAAGAGAGCCCTCGAGCGATCAGGG
ACCGACTCGGATCGCTTTAAGGCAAGATAGAGGATAAATATCTGCTTTGGAAGATAG
TCGTAATCAATTTCCATCTCTGTTGTTTGTGATCTTTCTGCTTTGACTTTTCTTTC
CTACGCGCTTTATATAGCTATGATGTGCAAGATCCATCAATTTATGACTGGAAGA
GAATTTTCCATACCTGCCACAGTAAGGCCCTTCAGTCTACCGCTAAGAGAGCTTAACTA
TCCCAATTTTGCCTGATTACCCAGAACACAGTGTGTGTAGGGCACTCCCAATGATG
CTTACGCTCCCTCCCTTGAGATTAATATAGAGGCTCATACCACTGATATGGAAGAAA
TCTTTGCTGTGCGGTGCTTCACTGGCTAGCGGCTATGCTGACACCGGTCTGTTAT
CCACTGACGCTGATTCTTCTTCTGCTATGCTTTTGGGATATGTTTACATGGAATTTA
ACTCTGTATCACCGATATATTTCTGGAAGAGTTATGTTGTTGGCCACAGTAGCCCA
TGTATATTTGGGCTGTGCTGCGGTCTCCCTTTTGGAACTCTATAAATCAGAAACCG
AGAATGATGTTGTTGTTGTAGTAAAGTCTATGCGGATCTTCCGAGAAAGACAACA
GTCAAAAGATTGAAGCAAGAGTAG

>YDR178w, 181 aa (SEQ ID NO 106)

MLPRSNKFMTRGRIFHTATVAFQSTAKSLTIPLPVLPLQKPGVGRTPNDIVPPPE
NKLEGSYHWMKIFALSVPLATAMLITGPLSTADSFVSNLLGYCYMEFNSCITDY
ISERVYGVHVKVAMTLMGLGSVSLFGIYKLETENDGVGLVLSWDSSEKDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAATTCCAACCGGAATTTGCAACAGCAGCAATTTCTCGTACCATGAAGGGGAACATGG
CGCTGTACAGAGGTTCATTTGGCGGAGTATTAGCCAGGCCCTTAATACGTAACCTCGGTA
CGCTCTTACGCTTCTTTCGCAATAATCAAGTCTCTGTTGTTATGTAATCACTCACAGTTCCATG
GCATCCGCCAACCTTGTCTCTTACCATAATTAATAGAGCTTAAGGCTTACATTGCCGCC
GAGGTAAATATTAGCCACAGCTTGGCATTTTCACTGGCAAGTAGCTGTTGATCTCAGT
AAGATTAACCTCAACATACTCTTTTACTTGTCTCTTTTGTAGTAAATGCTTCTCTCC
CTTCTTTTCCACAAACCCCACTATTTTCTCTCAAAAGTTATATGAATATATATATCTG
AATGGAGCAATTCGGGTGTAGTGAATTAACAAATATATAGTATCTGATCAAGCACACAGT
GGAAGTGTCTGAAAGCAATATAGAGTGTGATTTGTTTCTCAATATAGATTGTTGTGAG
AGATAAATACGACAACATTTAAGGATCGGCTTAAAGAAATGCTCTCGCTCATCGAAGAAA
TCGTCAAAACCCCAATTTACCACAATATTGACAACATTTTCTTAATGTCTAGAGATGCTAG
AGAGTGACCAAAATATCAAAATGCTGTATCTAATGTTATTTCCAAAGCAATACAAAC
AAAAACGCTCTCCGACGTAAGGGGTGTATCACAGACAGGCGCAATACATTGTTGACT
TTTCAATGTTGTGAGATTCCCAATTTCAAGGGGTAAACAAGTTTATGTTCCGAAATGA
ATACGGGACTGAATTTCTTCTTATCTTCAATTCAGTAAAGATAATGACCGCACTTGAANAATA
TTTTTGAATPACTGAATCACTCAAGTAGTACAGATGTCAGCGAATTCGTATCCCAAT
TTTGGCGTGGCCATCGAACTTTTGAACCATCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGTGATTTCCCAAGAGTAAACATTTGCTATGTAAGGAATGTTCAGGATGTTTACT
CAGTCTGCGAATCCACAGATCACTCTTAGGACTGGAACCTTACGCTTTAGGATGAGC
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTTAAACCTTGTGTGCGAGATTGATA
GTAAACCTGCGAGTCTATTTTTCGACCAAAATTAAGAAATCAAGTGACAAAATCGAAGAAACA

73/251

AAACTTTATCTAAGATCTCTCAGAAAACGGGTACAAAGTCCAGGATTCACACATTACTTA
ACCACATATTTCTTCTTCAAGTGAAGCTATAACACTTCCAGAGCTCAGAACTATAT
TAAAGAGGGCGTTACTTTTCGATAATAGGGTAGTCACTGGAATGTGAAAAGTTAAATATAT
CTCAAGTGAATCAACTTTGATCATGATATAAGCGCCAAATTAAGAACAGTCTCAAAAGCTTCGA
TGGCGAACCATCAAGCAAAATTTGCTAGTAGCAAAACAGTTAAGTACATATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLFPNDRFGABDKYDNFKAVKESWLIBEIVKPOLPNIIDNFSKCLEMLESDQIFK
MFVSNQINPESNKQNDSPTKGVITRQGVIVDFHVIVRFPQFORQKQVWFRMNTGLNFL
LIQFSIMTHLNLILBEILNQLQVATVSEFVSKFVAMELLNHLNLILQNPDPDLVFPED
NNFAMKEMFQDCVSVCESTAHILGLEJLTCRNLCEIELNLIKLVTKPKWCEIDSKGRSP
CDQIRNVNERNKTKLSKILSENGVQVQDSTLLNLHIISSFSQSEAITLPEAQELLRRGVTF
DNRVMECEKLIVSTSDPTLSISAKLNSLKASMANHQANLVAQKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGGCTCGGAGAGTTTTTGAAGAAGCAAAATAGATTCCTCGC
AAGTTTGTGAAGAAACCATCGACAAGAAATTACAAGGTTTATTTCTGATGAAAAGCTCTAA
CTAATATTTTGAAGAAAGTTGACAGAGAGAAAGAAAAGCTCTGTCAAACGCTCTTGGC
TGAAGAAGTAGCGGTGTTCTTAACCACTATTAAAGCCGCAATTTAGTAAATGCAAAAAGT
TGGCGGGAATTAAGCCGCGCAAGTTGTGGGGTCTCTTAATCCGAAAAGAGCGGCTTTAA
CAAAATATAAATCCGAAAATCCACAGTACAGAAATTTGGAGAAACAACACAGTTTGTGATA
TCGCCATACATATAAGAGATGTGAAGAGCATTTCTTCACTGTAAATGTCCTCAATACAT
TTGAATTTCTGTAGTGTATTTTAAAGGTAAGTAAATAATATAATATAGTACTTACAAA
TAAATTTGGAACCCCTAGAAAGTTCGAATTTGGGACAGAAAGAAAATAAGTAATTTACT
CTGATTAAGAGAGATAGATGTTGCACAACCTCCACTGTGTAATCCAATCAATGAACCAT
TTGTACCACAGTATTTGGGAACTGGGCCCTTTTGTCTTTGCAAGATTTATTAATTTAAITTT
ATTCTTTGGCTCTATTTCACAGGAAAATATTTCTTCAAGGAATCCACATGCTCATGTTT
CTGTGCTCTCGCTATTTTGAAGTAAACCGATGACATTAATGATATCTGGGGTCTGCTA
TGTATTGTAATAATTTGGAAAAGAAACGAAATGTCTTCAACAAGATTTTTCGACTGTGGGTG
ATAAAGATGTGCCGACAGGTTGTGATCCAAAGGGGTTTGGCCCAAAATTTCTACACTG
AAGAAGGTAAATTTAGATTGGGTCTACAATAATACACCGGTATTTCTTTATTCAGAGACCTT
CCAAGTTCCTCCTATTATCCACACAGAGAAGAAACCCCAAAACCAACCTTAAGGATG
CTGATCTTTTGGGATTTCTCACCACTCTCGAAATCAGGTGGCCATTCATCAAGTAA
TGATCTTTTTCAGACCGTGTACCCCTGCAACTACCTGATGATGCTATGTTATTTCTG
GTCACTACCTATAAATGTGCAATAAAGCGGAGATTGGCATTTATGTCGAAGTTTCTATCA
AAACCGATCAAGGAATAAAGAAATTTGACCATAGAAGAGCTACCAAAATTTGCGGATCA
ATCCAGATTATTCGCGCAGGATTTATTTGAGCTATTCAGAAATGAGAAACTATCTCTCT
GGACAGTTTATATTTCAAAATGACCGAAGCGGATGCCAAAAAATTTACCTTTTTCAGTCT
TTGATTTTGAATTAAGTATGGCTCAGGGCAATTTCCCTTTTACGGCGTGTGGGTAAAGTTG
TTTTGAAGAGAAATCCACTGAACTTCTTCACAGAGTGGAAACAAGCTTCTCGCCCGCA
GTACCCAGGTTCTTATCAAGAAAGCGCTGATCCAGTATTAACAGGCCGCTTTGTTTTT
CATATGGGATGCTCATAGATACAGCTAGTCTTAATCTTCCATCAAAATGACCTTAAACG
GTCCATATGCTATATAATTTTCAATTCGCTATACAGATGAGACCGATGAATGTTAACTG
GCAATCTGGCTCAGAACCTACATATTTGGCCCAACGATTAATCGTACACATATATCCAAAC
AGGACACACCATTTCAACAACACAGAGGTATGGAATGGGCCAGCTATCTCCCTTATCATT
GGCAACATCTCCAGGTAGATTTCTGTGCAAGCAAGAAATCTCTACGCGCTTTTGG
GTAAACACCTCGAGCAAGAAACTTGGCATATAAATCAATCGGCAATTCATGTAGAGCGG
CCTGTCTCAAAATACAGCAGCGCTTTATGATATATGTTTGTCTGTTGATGAAGGAGCTAT
CTGAGGCAATTAATAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTCGAGTAACTCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGQEKNEVNVSDREDRVVNTSGNPINEPFTVQRIGEHPFLLLQDYNLIDSLAHFN
RENIPOBNPHAGSGAFYFVEYFDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADT
VRDPRGFATPHYTBEGNLDWVYNTVPVPIIRDPSKFPHFHTQKRNPTWNLRDADWFDF
LTTPENQVAIHQVWILFSDRGTPANYRSMHGYSGHTYKWSNKNQDMWHYVQVHIKTQGIK

74/251

NLTIIEATKLIAGSNPDYCOODLEFALONGNVPSTVTVIOTTEEDAKKLPSVSVDLIHW
 PQGEPFLRVRGVKILNENPLNFAVQEOAFABSTTVYPIVQASADPVLQALFVYADAR
 YRLGNEPHOI PVNCPYASKFEPFNALRGPMVNGNENFSEPYLIANDKSYYTII QDORP10Q
 HQEWNGPAIL PVNMAVS PGVDVQAGNLLRVLGAKQPEQOQKMLANIGIINHGACPCP10Q
 IVYDYPARVDKGLSEALKYVAEKHABELSNSKF

>YER103W, 2429 bp, CDS: 501-2429 (SEQ ID NO 145)

76/251

ATAATTGCAAAAACCGAATGCGCGCCGCCCTCACCGCAGCGGACGAAAGAGCGCGCGT
 CCCCTGTTTCTGCTTTGCGCTCATCTCTTTGGCTCCGACGCGAGCAAGACGGGATCCC
 CCTCCGCTGCTTTTATATAAACAAGTCTCATCTCTGCTCTCTTTGTTTCCGCTC
 GTTGCGGTACATGCGTGTGATTTATCCCAACCCCAAGAAAGAAAATTTGCTACATCTCA
 TCTGCAGCATTTATTTACCTATACCTTTTCCATTTTGTAGCAGATTTGCAAGTGAAGATAT
 ATCAGCATCAAGATATPATGATGACAGAACTTACTCTTTAAGAAATTTCCAGGACCTTA
 CGGCTCTCAATTTACAGAACCCCGCCACCACCATCTACAAACCAAGGTAGATCTTTG
 GGAAGGGTGGTGTAGCTTACAGCTTTTAGGAGAAGTCTCTGAGCATTTGCGCCAGAAAT
 TATCCAGAAAGTTGCTCAATTTGTTAAGATTGAAAGAAATGTTTTAGAGTCCATGGAAT
 TGACAGCCAAAGAACGAGCTGACCTGCTAAGCAATTTCTATTTTGGGGTTGGAACACG
 ATGACGATCTTTCCGACATCACTGATBAATTTAGGTGCTCTGATCTATGAATTTAGTGAAT
 TAGACGAAGATTTATGCTGTTATGACCAATACAGATGACTCTAAAGTCCATCAGAG
 ATATCGAACCTTTGTTTCAACCTCTAGACAGCGTAAGCAGACAGATCACCGCAAAATCG
 CCTACTGGAATACAAAGATCTCAATCACCTAAGATTTGAGGTCTTGGAAACAGAAATGG
 TCGGTCTGAGGCTGAATCTTTGTGCTGAGCTCAATTTATCTAATATCACAGGTCAA
 AGTTGAGAGCTGCTTTTCACTACCAATTTGACTCCATCATGCAATTCAGAGAAAATGG
 CTTTAAATCGCTGTAGGTAAGCTCTCTTTGGAACATTTGGACACACTCTCTGTCACCTC
 CAGGTGAAACCAAGCGCTGCTTAGCATGGGTATGAAGCCCTCTAAACAAATCATTTATGATG
 CTGAAGCGCACTGAATGACACTAGACTCTGCCCAAGTCAAGCTCACTTTAAGTT
 TCAAGCGGATTCAGGAAGCTTCGAACCTTGAAGAGCGCAAGAGAGGAGGAGAACG
 GTCAAGGCGGTGGTCCGAGACGAACAAGAGTGGACAAATTCGAACACCTGAACAAG
 AAGAAGAGGTGCTGTTGAAGAACATGAACAAGTCCGACACCCAGCAAAAGTGAATCTCTC
 CCCAACAAACACAGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPTAQLOLQPPPPSTTKGRFFGKGLAYFSRFAAGAFGLPSRLKLSQ
 LVKLEKNVLRSMELTANERDAKQLSINGLENDVSDITDKLGLVLYEVELDDQFID
 RYDYRLTLKLSIDISGVSPDRDKDIITDKIAYLKYPQSPKIELELVRAEBS
 LVAEALSNITSLKLRAPVQFDSIIIEHSEKIALIAGYKALLELDSDSPVTPGETRPA
 YDGYEASQKIIIDAESALNEWITLDSQVKPLSPFKQDYEDPEPEGEDEEEDGQGRWSE
 DEQEDGQIEEPQEBEGAVEHEHQVHQSESLEPQQTTA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCCAGTATGCCACACATATATGCTTCACACCTAAAGCACATATTTTCGTTATTTTTCAC
 CACAATAGTGTGATCTCGAAAGAGATGGAATAATCAGGAAAGAAATGTTGAGAAAAA
 TAAACCGATTCCTGTTTCTCTATTTCCGTGTATATGCGTGTATATTCGTTTTC
 GAATCTTTATGAATGTCGAGAGAGTGTACATCCGAATAGACTAAAGAAAGCA
 AAGCCGTGAGTTTGTATGATAGACTCGCAGCTTTGTCATCAACGGGCCACCTTA
 TTCCAGAAAGGCAATGGAACCGACTCGCGTAGTCAATAGCGTCTTCATATCTTAGCA
 TTGTTGAGAGATACATAGTGTACTCCATATCGTTCTTTTCTTTTATATATCAAGCCAC
 ATATCTCTGTTCTTTTAACTCTTTTATACCGCTGAAGATCGGGTACTGACATAAGTGTAG
 TAGCCGTACAGAGAAACAATATGACTAAATTCGTTGGTGAAGAGATCAGAGTACATTTG
 AGACCTCTAGTTTTCAGCAGCAGCTGCAATTTACTTGGCGGAGGACGGGTTTCTGACA
 GTAATCGCGATTCGCTAGGTTTCGGGCAATCTTCTGACTAGCAAGATCATTTAGAG
 ACTATCGGCTCTCTGATAGGACCGCTCTCATATGTCATCTGTCGGGGAAGTGGCGCTA
 ATGAGGAAGAGAGGGCGGTACGACGGGCTCCCTTGGCAAGAAATCAAAACGGGCTTT
 TTTTCTCAAGACTCGAAATCATAGGAATAAGATCTCTCGAAGTTGTTTGTGAACAAC
 TCTTCTGCTGTTGTTTGAAGTGAATAATTTGTTTACTTGGGTGCTCTGTTACGGAA
 CAGATCTGTTTCTTAACTGCTCATATCGAATTTACTTGGGTGCTCTGTTACGGAA
 CTTAGTTCATCTATTTCCCGATCATACCTCATTTGTTAGTATTCAGGATGCGGCATCTAATA
 GGCTATATACACCGCAACATCTTATAGGAATTTGTTAGCAGCACTCCACCGGAA
 TTGACAGAAAGATAGTCGATTAATTTAGCATGAGATATCTGCTGCGCTTTAAACGTTA
 AACCTTAATGCTACAGACACTTTGTTAATTTCTTTTGTAGTCCAGACGCAACCTCGGAGT
 TCAATTCATCAATTTTGTGAATCGGTGTGAAAGTGTGCGTGCACCATCGAGTTA
 AATCGACCAATCTTACCACCTCATGCAACAATTTGAGGTTCGCGCTTCAGAAATATTAGTCA
 AAGAAATATCTTCCCTCATTTGATGAGCAACATCATCTTAATGACAGAGATCTTAATATA

77/251

ACATGGAGAACTGGGCGATTCAGGACAGTTGTTGTTTACCTACACAGATTAATCGTCCCT
 TTGCTGATCGTATTTCTAATAGGCCCTCTGACAGTCCGCTGATTAATGTTATTTTGTAA
 CCGTTTACAACTGTCTATATATAGTAAAGTTGCACGGAGAAATGGCCAGAGTTCTGAAGC
 CAAAGCATATTTTAACTACAGCTTCTAATTTCTCTGGGCAACTTATTTCTCTCTTTCCA
 TTGGAATCTTTGACCGTATCTGCAATTTTATAGGATCGATTTTACCCCGCTTTTGGCAGAG
 GAGGATTCGTAGTATTTGGATGTTCTACGTGTTGTTGTTAATGATGGCTGTTGTTGGTGCCA
 ATGAAAACGTTTCTCAGCTTTAGTATATAGCTTACTGCCCCCTCCATACCTGAGTATTTGTTGA
 TGACGTGATCATATTAATATTTCTGCTTCTATCTACCCAAATGGTTTGAACAACGAAT
 TTTACAGTACGGCTACATAATCCCAATCCATAATGCGCGTGATATCTATAAAGTGAATTT
 TTTTGAATTTAAACCAAGAAAAATGGGAAGAAATTAACGGTATTTCTGTCGACATGGTTG
 CCCCAATACATCTCTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAA
 ATGCTATGCAAGCAGCAGACCGCGCTGTCGACAGCTTACCAGCGTGTAGCCGCCCGG
 CAGAGGCCCAATACTGATAAAAATAACAACCCCGCCGGAATTTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTRKSVGBESQVIEDPSFAAAAFTGGRDGVSYNQRFPAEGSGHSSDLAKSLEDYRPDE
 KPSLSVSGEGANEEKEGNDGGLARIQTGLFSPRLNRHKKILSKFVLNFFIACVC
 VSLISIVGACYGTDYFFKVNIVVLQDAPSNVSQSIISAIIPSLLASVPVTHIYNAT
 SFHRKFTGTSTEDRKIVDLYDERYMLALNVKNATDTLYNSLSQDANSEFNSSIFP
 ESVPESGRDPSVSKSTILPLMQQLEVRQLKYVKEVLPMSLNITSNDRDLNINMENWAI
 AGQLLFTYNDYRFPADRLMAPLQWGLIYCLLLTQLSLYGLHGEWAVLKPKHILY
 RLIIISWATYFLLSIGFTCSAISIFRIDTFPAGRGGEVYVMSTWLVMAVGGANENVLSL
 VIAYCPYLSIWLMTIILNISASFPYPMVLNNEFYRGIYIMPHNAVDIYKVIIFLNTKR
 KMRNYGILVNWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRPAAENTDK
 NNPPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCCTGTGTACGTACGATGTTTCTCCCGTGTCCGATTAATTAATTTAGTTCTGTTTCAACGGTCTC
 GCGCTTGATTCATTTATGCGCTTCTCCGGGAATAGTTGACCAAGGCAAAAAAATTCAG
 TCGGAGATTCCTTATTTGGCGGAATTTAGTAGATCTCTTTCGTGCTAATAGCCCTGCCCCG
 TTAGTCGTTATTTTACGCTTAACATTTTCTTGCCCTACGCTATATAAAATAACATACATAT
 ATATATGTCAGACACATTAAGAATCTCCCTTAATATTTGAATTAAGTAATTAATAGTTG
 AAAAGTCTTGTTCGAGGATTAGAGTGTCTTAATTTTATTTAGTTCTGTTTCAACGGTCTC
 AAAAAAGTGTGAACAGTAAGCAGACACACACATCCCAATTTACAGGCACCTGATTA
 AAAATCCAAAATTAACCATTAAGTTTATTTTAAATAAACATATATACGTGAAGACAAA
 CCGCATCAGAAGTTTTCAGGATGAATATTCAGAGAACCATCATCAGATGAAGTATATCTTA
 GTGCCCCGAGGATACAGATATCTGACGCCAGCAGACATCAGCGCGCGCAGAACGTGGAG
 ACCAATCAATAAATAATGAAAGAAAATCTTCCACTGGTCTTCACTGGAACAATTTGGCCA
 ACACAAATTTTAACTAAGAAATAAATGGCAGTTACAGAAGAAGAAAGATGATCATCT
 GCAACTCTAGAATAACCGATCAATAATGAGACACAATCAGCACTACAAAGGTATCTCCG
 TTAACAACCTCTGATACAGAAACATATGAATTTTCTCCGATACAAAGGAGTTACAGGTTTC
 TCGAACAAAATAAGACATCTATCTTTACAGCATGGAAGTCAAGATATGAGAAATCTT
 ACAGATACAGAGAGAGAGATGATGGAGATACGATACCGTTTTCGAAAGCAACATCTCA
 AGTACCCCAAGTCTATAGAAAATGCAATGTCATGATATCTCGGAAATTAATCTCAAGAGAAC
 CTATGGTACGATATTTGATAAATGGTGTGAGTGAACAAGCATGCACTAACACTATCTC
 CTGGAATAATTTTTCGGGGGAATAGCAAGAGCGTTTCTATTTGGTGAACATAAGTTTCT
 TATTTTCAAAATATGACCAATTTTATCAATGAATAATGATATATGATATAAAGCAAGCGG
 AACCTAACGATACGGGTTTCACTCTCCCTACCCCTGGGTCTTCAAGCTTCACTTTTGCATCA
 AGGAATTAATGGAAGAGCGGTAATGGCTCCACACTATTTATCAACTATCATCAGTATGATAT
 GAAAGGAGAGAGAAAGATTCATTTGGGACCATGTCNAAGAAACAACAATGATGATTAAT
 TCAGGTGCTCTTTTATAGGCACTTGGCTTATCAATCTCGAAAAGATAGAGACTTTGA
 TTACACCTAAAGAGTCTAGAGTAATCAAGAGAGTTATCAAAAAAGTTTTCGGGACT
 TTGATCATTTTATATTTCTTCCGAAGAGAGTAATAACAAGAGCAGTAGTTTCAGTAA
 GTTTCATAGAGGAGGCTCAGTAGAATCAACAATCTTCCCAATATATCTAATGAGAAATG
 CCCAAGATGAAGATATGTTGAAGGTTATGTTTCAATCAAGCTTATCAACCATCAAGCAAG
 CACTACGAGCCATCGAGACCTTCAATGTTGGTTCATGTTGGCATGGAACAGGCTCGTTGTTA

80/251

TTTAA

>YJL166W, 94 aa (SEQ ID NO 232)

MGPPSPKTYNGWGHMGPGKQKGTSTVAVSPYAKPLQGIHFHNAVPSFRFRFKSQDFLYVL
IPAGIYWMKNGNEYNEFLYSKAGRELEWRVW

>YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)

TTATAGAACTCTTTTATGTGTTTAAAGAGCTGTGTTATAGTAATCTAAGTGGAAATACACT
AACAGTAAATAGCGGTGAGCTGAGTGGTGGCGCTCCCTTAGCATGGGAGAGTCT
CCGGTTCGATTCGGGACTGCTGCCAATCTTTTATATCTTATTAATATATTTTTCCTGCCG
TTACTGCTCTTTTAAATAACTGCTCTTTATGAATACAGATATAATTTTGTATATACAA
GAGGTGACTGCTGATTAATCAATCTTAATTTGTGGTTATTTGGTACATATACCTTACAA
AGTTACCAACAACTGTTCGACTTTTAAATGCTTACCCGCTTCCGAGTGTTTTGAAGGGG
CGGAGGAGCGGCAAGAAATAGCATGGGAAAGAAAGCATAAAGAGCAATGGGTGGCAA
TGTATTAACTGTTCGAGAACTCTAGTGACTCAATTCATTATCAATACAAACAAGTTCCTCAAG
ATCATCGATTCAATATGTCATGTCGATGAAAGTATTAACCCCTCAAGTTGCATGGGCTC
AAAGTCTAGTACTACTGATCCAGAAAGAAATTTATGCTTTAATACTGTGTCTCAATTTGCG
ACTGTGATGCCCTGAGTTAACCATTAAGCCATCATACATCGAATTAAGGCTCAATCAA
AGCCTCATGTTGGGATGAAATGCTCATCATTAATCAATTTACATGATGATCTATACAAGG
AAATTTACCTGNAAGAAATGATGATGCTTAACTGAGCCAGCACTACTTTTGAAT
TGTATAAAGAGATTAGAAATCTGAATCTGACCGCTTTTCGACAAAGGAAAGGTGAAGT
ACCTTACATCAAACTGATTTTCGATTAATGGGTGTGATGAAGTCAACAAAGACGAAGTTG
AAGCTGAAGGTAAATGCTGCGCTCAAGAAATGGATTTTCAGCCAAATGATGGGAGGTGCTG
GAGGTCTGGAGGTGCTGGAGGATGACCTTACGCCAAATATGATGGAGGTGCTGTGGCG
CTGTGTTCCAGATATGGCTCAATGTCAGCAATTTATTTGGCTCAAGCGGTGCTAATTTGG
ACATGGGAGATTTCAAAGAAACGATGAAGATGAAGAGAGGAAATAGAGCCGGGAAG
TGAAGCTTAA

>YKL117W, 216 aa (SEQ ID NO 248)

MSDKVINQVAWAQRSTTDPERNYVLITVSIADCDAPELTKPKSYIELKQSKPHVGD
NVHHVQLHIDLYKEIPEKTMHKGQHVFLKYLKDLSEYWPRLTKKVKYPIKTD
FDKWDEDEQDEVEABGNDAQGMDFSQMMGGAGGAGGGMDFSQMMGGAGGAGSPDMA
QLQLLAQSGGNLMDGDFKNDENDEDEEIEPEVKA

>YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)

TTCAACGAAATCCGTACCGGAAAAACGGAAGCGGGGACAGTGAAGCGTGAGAGGG
GCGAGACAGGGGAACTTGAATGGGTATTTGCTTTTGTGCTGCAATTTTTCGCTGGTAC
CTCTATCTTTAGCGCACCGGAAAAATTCATTTCTCATCTTTTCTTTTCTTTTCTTCCG
ACTCGATACCTCTTTACAAAGAAACCCCGCGGGAAATGTTAGATTTGAGCTTTTCTCCG
CAGGAAAGAAAAACCTGGGACATTAATCTTGTGTTTTTCTTTCTTTCTTTTCTTTCTTCC
TTGGATGACTGCGAGAAAGTACAGTTACCGGCTTTAGCAAAACAAACATATATATAT
ATATATATGAAGCGTATGCTCAACGGTTTTATAGGTTTTTCTTTTGTGATTCAGTTTC
AACTTGGCCCTTCTTATCGCATTCAGATACATACACAACTGCTATACACACACA
AATAGATACATATACAGAAATATCATGTTTGGACGATCAATTAATTTCTGACCAGATG
TAAATGTTATGATTAACATCACTACACAAAGCTGCGATGATCTATTTCTCATATG
AATTTAATATGCAAGCTTGGAAATATCCGGCTTACGGACACTACTATTTGAAGATGCGCA
AACATAAATCTCTGATTTACCAAGTGTCTTCTCAGAGGACGCTGATGATTAACACATGT
ACCTCGTTAGGCTACATCATCTCCCTGAGGGGTGCTCATTAATACATTAATCTTTTAC
AGAACTCCAAATCCATCTCCATCACTGGAACAAAGCAACGATGTAACGGGT
TGTACCGTCCAGATTTGACTACATAGATAGTAAATGAAGCAATATCCCGGCTCCAGA
ACCAATATGACAGAAACAAATAATCTAAATCTGCTTTAAGAAATAATACGGAAAT
GCTGGGTAAACCGAGGAGTGGATGAGATTAACGCTTCTATAGAGCAATGACACGCTT
TGGTAAATTTAGAAAGACATTTCAATGCCATCTGTTGATTTCTCAGCACTGCTTCCATTT
TCGACCAAGCTTCTACATGCACTAAAATTTCTCCATAGTGAAGATTTGGAAGACCTTA
TGAACGAAAGAGGAAACAAATTTCCCGAAGTTGAAATTTAACCAGCGCTGATGAAGA
GGGAGATCGACTCAAGGGGACTATCCCGGAATCCCTCATCAACATAAACGATATCCAAAC

81/251

ATTTCCGCCACCATCCGCGTCAACATCGTCCCATCATCAACATCAACATCAAAATAGTTT
CTCATTTGATGAACAATAAAGAGACTCATATATGAGTTCAGCAACTATACATTTGGCA
CTATGGAAGAAGACATTTTTTTATAGGAACACAGGTGTGTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)

MTSLDDTTIISYQINIMLLDNMTNKNKPAIDYFHHFNDASLEISAWTLLKMKRKHLLRL
PSCSDEDVLDDYNNYLVLRLHCLMRRWSINHYGQNSKSNPLSINNKETDVTVLVYGPDLT
NIDSNENETSPQNOIDOKQTNLKSALKKNTCEWTEVDEINASIESNDNALVKLEDI
SCPSSVDSHTSIPDQHSCTCKTSSIDEDSEDLMEKEQFPRLKFNQAVMKREIDSKG
TIRPSSILINDIQHSRRHRRHRRHHHQNSSHSDETIKEAHYEPFNYTFTGTWEEDIF
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)

GAAGATACAAAGAGGTCCAAGAGAGCAAGACCCGATGTGTGGGACACGAGAATATCC
AAGACCGGATGCTAGTAGAGAACTCTGCATACAGCTGTGCCATGCCGAAACAGGTGAC
TGGAGCGATGCTTCAACGAGATGGCTTATTTAGGAAGTGTGGGAAAGATATGTTAAT
AGAGACCGGTAAGCACAGTGGACGTGGATGGGACGACCACTAAGGATTCGGAAAGAAAG
AAATGAATACTAAATGTGTGATTAATCTTGTATATATATAGACAGCTGCGATGATCG
AAACATATGTTTCCCTTTATAGAACATACTGTACGCTTTTGAACGGCATTTTATATGA
GCTTCTAGAATAATTTTCCGCTAGCTGGAGAAAGTTCAGACAGAAAAATTTTAAATA
AGTCGAATATCAGAGGTGCTGATGCGCTCACATACATAGAAAACTTGTAAAGACAAAT
CAGCGCAATACAGGAGTAAATAGACTAGACTTAAACCTTTTGTGATATTTCTATTTGGAG
GTAAACCCAAAGCCGTATGATGTTTTTGTGTTGTATCAATGACATAGTGTCTTAAACGGCTG
AAAATTTTGAAGTTGTGTGAAGAAATCTGTGTATGGCAAGCACTAACTGATGTAC
CATTTGCTGACAGGGTCCATTTTCCACAGATGATCAAGAGCTTTCATGTGTCAATTTTG
GTGATTTTACCAATTTTAAATGTGTACTGGCGGTGAGACATATACGATGAAAAATTCGAGG
ATGAAAATTTCACTGTAAACATGATAAACCTTTCTTCTATTCATGCCCAACGCGCGTCC
CAAATACCAATGGATCTCAAGCTTTCTATAACCTGTGTCTTCTACACCTATTTTGGAGGGA
AGCAGTGTGTGTTGGTGAAGTGAATCAAGGTAAAGAAATTTTCTGTTGATGTAAGAAC
AACAAATGACCAAGAAACAAACAAACCCATTTGCTGTGTATGAAGTATGATGCTGGCG
TGTACTCTGACGATATCAAGTCCGAGAGATGCGAAGCTACACCAACAGATGATGATG
CGGATAATATAGACATGTTTTTAAACAGACGAAAGTTGACTTGAAGATTTTCGACA
CCTGTTGAAAGCTATTCGAAACGTTAAGCAACATGTTGACTGTAACAGCTTCAAGAAACAGA
ACTATCTCGCTGGCTTTAGAAAAATATGTCAATGTGTATAATTTCTTGAAGATTTTCC
CAGAGATTTGGAGAGGAACAATTTGAAAAATCAATCAATTTGAAAGTGTCTATTTCCAT
TGAATATTTGCCATCTGTGCTCTTAAATTAAGATTTACAGCAAGTATTTAGTACCTCAT
CGGAGGTATATATGCGGAGCGGTGACAAAAAGCCAAAGGCCAAAGCTTTGTACCGTCC
GTGGCCTGGCTATTTACCATGTTAATGACACAGATATGGCTCTCAATGACCTAGAAATGG
CCACTACTTTCCAGCCAAATGACGTGCCATTTTGAAGCTATTTCAATAATTAATAATTA
AAAGAAAGCAACAAAAAGCAAGAAAGCTTCTTCTTCTCGAAGATGTTCTCTCTCA

>YLR216C, 371 aa (SEQ ID NO 280)

MTPEKTFPDISIGKPGQRIIVPELVNDIVPKTAENFLKICEGNAGMAKTKPDVPLSYKGS
IFHRVINDKFCQDFGFWNFGTGGESIYDEKPEDENFTVKHDKRFFLLSMANAGPWNQSQ
AFTEVPTPHLDGKHVVEVIGQKRIIVRLIENQOCDQENNKPLRDVKIDCDGVLDPDYQ
VPENAEATFDGNDYDLKQDEKVDLKNFDVLKATETVKNIGTEQFPKQKQYVVALE
KYVKCDKFLKEYPEDLEKEQIEKINQKVSIPLNIAICALKLKDYNQKVLVASSEVLVAE
AADEKAKAKALYRRGLAYVYVNDTDMALNDLEWATTFQPNDAAILKAIHNTKLKRRKQNE
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)

CTTATCTCAGGTACCCATAATTTCAACCATCTTACCTAGCTTCCATTAAACACACATGAGT
TTCGTTACTAGCAGAGCGGTATCTGTAAATCTTGTCTTGGTTCGAAACATCTTAGCTGAAG
TGAAGAGGACAGCGACCTGCTGAAATGCTCAACGTTTCTGTAATAATCCGCTATTTCCGC
GGAATCAATAGGCTCTTAGCAGCGCCCATCAATTTTTCAGCGTGGCGCATTAATAATTA
ATTACCAAGATTTTCCATTTTCCGCGCTGATTTCTTATCAATATTAAGTAAATCAATCTTTTC

84/251

GAATTGGTTTGGTGGTCTGTTCTGGTATACATATGTTGGTATGTTGATTCATAAATTCGCTT
CTATGACAAATGGTACCAATATTTATGTTGGTAGAATATATCTCTGGTATGCGTGCTCGTG
GTATGCTGCTCTATCTCAACTTGTATTCGGAACAGCACAAACACATATGAGGTA
CCTGTGTTCTCTATCATAGTAAATGACACCTAGTATTTCTTAGGTTACTGTACCA
ACTATGGTACTAAAGATCATCTCAATCAGTTCAATGAGAGTGCCTTTGGGTTTGAAT
TTGCTTCTGCTATTTCTATGATGCTGCTGATCTTAATGTTGCGAATCTCCAGATCT
TAGTCGAAAAGGAGATACGAGACGCTAAAGCTTCTTTTGGCAAACTCAACAAAGTCA
CCAATTGAAGATCCAAGTATGTTGCTGGAATGGAATACAAATTAATGACCAAGCTG
AAAGATTAGCCGCTAACGCTTCTGGGAGTATTTCTCCAAAGAGTCTTAATTTAC
CTGCTGATTAATGCGGTATATGTTGATCTTCAACAAATTAACCTGGTAACTTACT
TCTTCTATATGATGACTACTATTTTCAACGCGCTGCTGATGAAAGATCTTTCCAAACTT
CAATCTGTTTAGGTATAGTCACTTCGCAATCCACTTTCTGCGCTTATACACTGTTGATA
AATTTGGTCTGTAAGTCTATTTGGGTGTTCTGCTTCCATGCGCAATTTGTTTGTTA
TCTTCTCTACTGCTGCTGCTCAAGCTATATCCAAATGTTAAAGATCAACCACTTCCA
AGCTCCGGTAAAGTCATGATGTTCTTACCTGTTTATTCATTTTCTTCTCGCTATTA
GTTGGCCCAATTTGCTACGTTATGTTGCGCAATCTATCTTTGCGGTCTCAAAATC
GTGCTATGGCTATTTGCTGTTGGTCCAACTGGATTTGGGTTCTTTGATTTGGTTCTCA
CTCCCTTCAATACAGTCAATGCTATTTTCATACGGGTATGCTTTCATGGGCTGTTGG
TATTTTCACTTCTACGTGTTTCTTTGCTGCTGGAACCAAGGCTTAAACATTAGAGG
AAGTTAATGAAATGATTTGAAGTGTCAACCATCGGAATCTGCTAGCTGGATCTCAA
AAGAAAAAGAGTTTCCGAGGAATAA

>YMR011w, 541 aa (SEQ ID NO 304)

MSEFATSRVESGSGQTSIHSTPIVQKLEDESPIQTSKSEYTNABLPAKPIAAWTVICLC
LMIAPFGVFGMDTGISGVNQDTKRRFGKMSDGYLYLSDVRLTGILVIFNIGCAFQ
GLTGLRGLDMYGRIRIGLMVVLVIVIGVIQIADSSDKWYQYPIGRILISGMVGVIAPLS
TLISETAPKHIRTCTVSFYQLMIFLIGYCTNYGDKYNSVWRVPLGLNFAFIEM
IAGMLMVPESPREPLVEKRGVEDAKRSLAKSNKVTIEDPSIVAEMDTIMANVETERLAGNA
SWGELFSNKGAILDLPRVIMGIOISLQKLTGNVYFFYGTITFNAGMKDPSFOTSVILGIV
NFASTFVALYTVDFGRKRLCLLGSWSAICFVIFPVGVTLSLXPNKDKQDPSKKAAGNV
IVFTCLFIPFPALSWAPIAVIVIAESPLRVKNRMAIAVGANWIMWGLIGFFPTPITSA
IGFSYGVYFMGCLVFFSYFFVFCETKGLTLEEVENMYVEGVKPMKSSSWISKERVSE
E

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTCACCTCGATCTACATATTTCAATGCGAGATGATTAATCTTCTGCCATTTGAC
AACAAACCTTTTACTGCCAGCGCTTTCATACCATGATGTTTATATGCTCTAATTTATA
ATAAAGCATGACATATAATGCCAACCCCATATTTATATAGTTTAACTTGAAACCGAGATT
ATCTATTGCCACGAGAAAGTGCCTTCTTTAAACATAAGTTACGTACCTCCGACCAATTCA
TCTAAACCGCATCAATCATTTGCAGCAGAGAAAGATGTTGTTAGATGCTCCTCGTTCGCTAG
ACGAGTCAATGATACAAAGTCTTTTCTCAAGCTGCTTTTCCATATAAAGGATTCGCAA
ATGGGCTCACCAATAGCGCTTTTATTTTTCACGCGCAAGAAACCTTAGTAGCTCCCTAG
AAATGAATAAGAGGTGATCTGAGGTTCATATAAGCTTTTGGTAAACCTTGAACCAAG
AAAGATTAAACACACAAAGCATCTCCTATCAAGAAACCTGATAAGAACTGTTTGTGACTC
ATCCAGCTGATGAGACACAGGCTTCATATTTCTAAAGTACGCTGCTACAGTTTATTTCT
GGAAATTGAATCTGAAGACAGTGTGTTGTTCTACTCTGTTAAATAGGATGTAGCA
AACCCTGAGAGGTGATACCTTTGGTCTTCTCTGTTATTCGGGAAATAATAGCACCGATG
AACATTTAGTGAATTAATACCTACATAGTCTTGAAGAAATTTCTACTTTGGGAGTTTGG
GTCAACTAAGAAACCCACCGACCTGATCAATTTGGCTTGAACCGAATAATGCTTAACC
CAGAAATTTGACCAAAATTTGGGCCAATGAGTATCTTTGATTTTGTACTGTTGAATTAGGCT
CCGATTTTGAATAACTGCCATAGAGTAGAATAACACATCTAGTTTCAAGGAATTAAGT
TCAACTGTTGTTTCCATACATCTCTCGTATCGAAGATATTTGAAGAACAAATGTTCTCTA
ATTAGCTGGCATGAACCTTTATGACCACTGTTGAAGGAATCTTACGTGCAAGAACCC
CAGTCTTTTACCTTCAATGAAGAACCGATCTAATTTATCAAGATCTGTCGCGCGAAGCGG
CCATTCAAATAGTTGACAGAGGGGTTCAAAATTCACACTCTTAAAGATATACAACTTGGCCG
ACACTGTTGTTTGGAAATCAATGATGAGAGTCTCAAGGATGCGCCATTTTCGAACCAA

85/251

AAACTGGTTTACCAACAAATGATATGTAATGAACTCTGGTCAATGTTTCATGATTTTATTCCT
TGGCTCTCGTGAATAAAATGGAATGCTTATCAATTACTTTTGCAAAAGAAATTTGAAATATC
AAGCTATTCAATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MFIKETDKVELTHPADETTSSVHLKYGATVYSWKLSEBQJMLSTAALDKSGSKPVRGGI
PLVPFVFGKNSDDEHLSKLPQHGLARNSTWELGQTKENPPTVQFGLKPEIANPELTKLW
PNDYLLILVELGSDYLKTAIEVENTSSSKELKFNMLFHTYPIREDIEBGTVMVSNLAGMKL
YDQLKESVVDKHPVVPFNOETDVIYQNVSAERAIOIVDKGVQIHLTKRYNLPTVTVMNP
WIEKSGMADPEPKYGVQMICIEPQHVDPISLAPGKKMNAYQLLCKEELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGAGAGAGAGCTAGATATATATACAGCAGCCACATAGTATACCAAAATTCACGATACAG
GCACACGAGACATGATCAAGACACTTAGAGGAAATGGAACAACGAATTTCCAGCCAAAA
ATTTCCGAGTAGTTCATGATGAAAGATTTTACATGCAATTTATATATAATATATACCGT
CCTATATGATTTTATGCAACAGGGGTATATAAGACAAATTAACCGGTGATGATATAT
CAACTATCGACTCCCAAGCTTTTATCTATCAGTCAATTTTACATCAAGATCCCACTTTTA
GATAGTTCGCAAAATTTCAATCTAATATATAGTATTTAATATAGATGGTGGATTTGCTTACCC
TTTTTTTGTGCTTTAGGAGGAGATTTCTTCCGATTTTAGGGATAAACGGATATCTTAAACCATAGC
TATATAAAACAAACCTTAGGCATATTTGATTTCTTAAAGGAATATTTCTAAACCATAGC
CATAGTAATTTATACCAACATCTCAACACGCGCTCAAAATATTTGAATTTATACCCAG
TGTCTAAATATAGATGAATATGTTGAAATCTCAAGAAATTTCTTCTTGGAGAAACAAATGA
AATGTGCCACCAAAATACCAAGGAAAGAAAGATCTAGAAATTCAGGCAGTTGCGAGTTGA
AAAACTCTATATGCGCTCAAGAGTATGAGGAAGAACTGATCGATGCTATGTACAAAG
ACTTCTACGGAACAAATTTGAATCGGTTCTGAAATGAAACGACCAAACTTATGAACGATA
TACTTCACTAATGAGATTTTACCAAAATTTGATCAAACTCCGAGAGATATCTGATCTT
CTCTCTCAATTTATGTTGTTGTTAAACAACTCTGAGAAATATCAAGGGCGAGTCTTTGA
TTATGTCTCTTCAATTTTCTCTACTTTTACATTTGCCCCATTTGCCCATTTGCCAGCTTTG
CTCAGGTAAACCACTGTTCTGAGCAGAGTAACTTAACACCAACACACACTGCTGTTAGTTA
TGGAATTTGTTTAAACAGCTGTTCTCTGATGATTTGATTTCAAGTATTTTCAAGGAG
CTATAGATGATTAACAAGACTACTAGATTTGGAATAATTTGACCTAATATTTCTACACAG
GTTCTCCCGTCTCGATCAATAGTTGCTGAGAAAGCAGCAAAAGTCTTAACACCTTTG
TACTTGAACCTTGTGTTAAATCACCCTACTCTTTATTTACAGAAATTTTCAAGCAAGTAACA
TAAAAATTTGCTTTGAAAAGGATTTTGTGCTTTTCCGAAATTTCTGGCCAGATTTGTG
TTTTCCAGCATTTATTTGTTGATACATAAATCTATCTATCCAAAGTCAATTAAGAGTGTG
AATCAGTACTATAATGAAATTTTATCAAGCTTTTGAAGAACAAACAGATTTTCACTCGTATGA
TTCTAGAGCTCTTTACAAAGGCGTTGCAAGTATAACTCAACTAACCGCTTCCACCAA
TTGTGCTTCAAAATTTCTATCAATTCAGATCTGAGGATCTATGCTCTTGTATCCACCAA
CCATGTTTATAACAATTTGTTGGGATGATCTTTGATGAAACAGGAAACCTTTGCTCTCTG
TATTGCCCATCTTAGTACGAGGATCTTTGATGAGACCATTAACAGATTAATAGGAAGAC
ATGACACTCTTGTGCAATACATATCTCTGATAGCCAACTGAAATTAATTCGTAATCT
TGAGCGCTTAAGATCTGCTGACTGTTGCTGGTGATACAGTATGATGATTAATAGGAATTA
CCGACGCTCAATTTGGAGGATCGGTACTTTCAGGTTATGCTTAACATAATGGAATATATG
GATTCATATCCTTTAGTCAAGAAACAAATTTTAAACAAACCATATTTGGAATGATTTTA
CCCTTTTATGAGATACCTTCCAAATAGCGCAAAAGGAAAGAGTCTGCTCGCTTTTGGCA
TGGAAGAAACACCTTTGTTGACAGAAATGGCAATTAACAGTGGGGGTACGCCCAATAT
TTTCAATATCTGCGCGCTTTTAAATTTAGTACCATTTTACGCTCATTTGTTCTTCTCTGA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNTPYPSKIDIEIVEISRNPFKQDKLKHSHENNRKXDLBFRQLQKLKLYYAV
KDHHEELIDAMYKDFHRNKIESVLNETTKMLDLHLIELPKLIKPRRVSDDSPFPFNG
KTIVKISRSVLIAPNFPFLLAFAPLAAALAGNTIVLKPSELTPHTAVVVMENLLTT

86/251

AGFPDGLIQVAGDAIDETTRILDDCCFEDFYFNGSPRGISVIAKEAAASLIFCEVLGGR
SPTTEITFNKASINIKALRIFFGAFNGSQCICSPDILYHKRSPVAVICEVUNEEF
YSPFEEDFETFMHIEPAKRAVASINSTNGSKVPSKISNSTEDLCVPTVIYNGIG
WDDEPLMKENPAPVPIIEEDIEDETINKIEEDHPVQVAFSSQSEINILLRNRSG
DCAAGKTVTHVGTIATPFGGIGSGYNGCYGVNFSEHRTIEQYMDNFTLFRMYR
NSVSEKYLVRAMEKRPWMDRNGNNKGLRQYLSLSAAVLLISPIVHCCSS

>YMR173W-A, 1685 bp, CDS: 501-1685 (SEQ ID NO 691)

[illegible]

>YMR173W-A, 394 aa (SEQ ID NO 692)

KFDLDFDKNNILLCDLUSMLDCMSCGVSAGK
 IHTPAATTVTLVPTMTTLVHVLPIETRPMSGLPTVHPTMTLHVLLEAVLINTVTVTL
 VLMVPTMTLMTLMTMLHVLPIETRRVLMVTLIRAVLVTMLPIVLLTKRRVLMPTMT
 VLTMTIRAPATMTVLVPTMTTLTVQOTRIRALVTALMTMLDPLPTTLTVPTTRBR
 ALMTMLIHAVLPRTRRVLMVABATIRAVLVTMLIHAVLTMLHVALMTMLPTMTIRALM
 NVLTMTIRAPATMTVLVPTMTTLVPTMTTLTVQOTRIRALVTMTIRALVPTMTLMT
 MTMTPTPTMTMHVLTITLHVLTMLIHVALTMTMHAPMTMTMHMLTMTLPIVLPRTRRAL
 KFDLDFDKNNILLCDLUSMLDCMSCGVSAGK

>YNTL031C, 911 bp, CDS: 501-911 (SEQ ID NO 325)

CACACAGCCCCAGGGCGCGATGCACACATTTTAAATTAAGCCCTCTTCTGATCGTTGTTT
 GTTTCCTGCTGCTGCTGCTGATTTCTCGCGAAAAGACCTTGACGCGAAGCTTCCGAGAAC
 CTCTTCGCTATACATTCGCGAAATCTTCGCGTTAGTACACTTCCGCTCCGCGCCAAAGCGA
 TTTTGCCCATATCAAAATGCGAAATCTTCGCGTTAGTACACTTCCGCTCCGCGCCAAAGCGA
 CAGTTGTCGCGTTCGCGACACTTCCCATTTAACCGCGGTAAACTATTGTCAGCGCCCTTAAGG
 GCTCTTACGAGTGGGAGTGGTCAATTAGACCTTATTCGCGCATATGTGACGACAAATC
 ACGTGCATGCGCTGCTGTCAAAACAATAGTTTGGCGTATACACGCTGTGGTCTGCTGCTG
 CGTGGCTCTTGTGAGACCGAGCTGTAAATATATCTTTCTGTTCTTTATATATAGG
 ACCACAGCTTTTGTGACTTCCACTTTGGCCCTTCCAACTGTTCTTCCCTTTATCAAAGG

WO 02/064766

PCT/EP01/15398

87/251

ATCCAGCAGAACATCTCCACATATGGCCAGAACTTAAACAAACAGTAAAGAAATCTCTGGTG
GTAAGAGCCCCAGAGAAACCATATTAAGCTTCCAGAGGCTSCAGAGAAATCCGCCCATCTACCG
GTGGTCTTAAAGAAAGCCCTACACAGATTAATCCAGAGAGTCTGGTCTTACAGAGAAATTTAGAA
GATTCCTTAAATATCTCTAGCATGTATATAGAAAGTATCCCTTCCAAAGATTTGGTCAGAG
GATTCCTTAAATATCTCTAGCATGTATATAGAAAGTATCCCTTCCAAAGATTTGGTCAGAG
AAATGGCTCAAAATTTCAAGACGCACTTGAGATTTCAATATCTTGTGATCTATGCTGCTTTGC
AGAAATCTGCTGAGACATATCTTAGTCTCTTGTTTTGAACACATATATGCTGCTGCTATATC
AGCATGAGGCTGTACTATCCCAAAAGAGATATCAATATTTGGCCAGAAAGTCTAAGAGGTG
AAAGATCATGTA

>YNL031C, 136 aa (SEQ ID NO 326)

QKDKDILARLRGERS
LILRIKLPIFOULVEIØDFETDLRFOSAGALQESVAYLVSLFEDTNLAIAHAKRVTTI
MARTKOTARKSTSGKAPRKOLASKANKSAPSTGVGVKKPHRYKGYTALREIRBPQKSTE
ZANBOY

>YNL134C, 1631 bp, CDS: 501-1631 (SEQ ID NO 331)

AACTCGGAACCTCTTTTCTATTCATCTCCCTCTCTGACGTGCCACAGGAACCAAT
AAAGAACCGAANATACCACACCCTGACATGCTCAAGCAATTCATGCTTACATGGAACCTC
ATTCTGGTGAATGAATGCGAACAATGATGATCAATGATGCTGCTCCATCTACCTGTC
GCAATTTTAAATGATCAATGCGACAGCCCTGCTGATCTAAAGTCTCTCGATCCGCTTACG
TTCTCGCGCGGTCCGCCCTGCGTACTCTTAAGTACTGACGATATGCGCTCTCCCTGTTG
GATTGCGATGATTAAGTAAGACAGATCTTAAAGATTAAAGACCGTTTAAAGTATTTTC
GGAATATCTTCGATTAAAGAGAGAGTTTTTTTGTGCGTTTCTCTCTCATCTTC
TTGATTGTAATGTAATTTAGTTTAAAAAAATGCTTAATCTATACACAGCAAAAAAGCA
TATCATACTGCATATCAAGCATGTCCGCTCCGATCTCCAGAAACATTAAGACCGTGTCTA
TTGAAATNGCAGCTGTACGTACAGACAGCAATCTCCATCTTCCGATTCTGMAATTAGAAAGGAT
TTGTTCTTAATTAAAGCTGTGCGCTTACCGGTAACCTCAATCCGATTGGAACATATTGATT
TCAAGATTGTCTCACAAGTGCCCTCTTAAGCTGTATGATATCAATTAAATGGGTTATTTC
TTGGGCCAATATGTGATGCTGACCGCTTCCCATATGCGTGTATGCAAGCCGCCAATATCGTAAGT
ACGGTGTCTGCTAGTGTTCCCTCTAAACGCTGTCTTGTCTGATGATCTCTGCAATTC
CCGAGATCTGCTTAATCAACGACAGAGTTTATGATTTGTGGGTAAACACAGCTACAG
AAGCCCGGTAAATCTTTTAAAGGGGCAATGCCATGCAATGGAAGCCCTTCAAAGCGCAAT
GTATGATCTTACACATATTTTGGGTGTGACAGTGCATGATGGAGCCAGATGCTTATTCAT
GAGATATCCCAATCTTATTTTGGGGGTGCGCACTGCGTGTGGCCAGATGCTTATTCAT
TTGCAAAAAACCACTTATTTTGGGGGTGCGCACTGCGTGTGGCCAGATGCTTATTCAT
TTGCAAAAAACCACTTATTTTGGGGGTGCGCACTGCGTGTGGCCAGATGCTTATTCAT
AATGTTTAAAGAGTACGGTGTGACATGATCTTTTGTGACTACAGATGCTGTCTCCAAACAG
AAACGATTAATAAAGAAATGACACAACTCTCTTACTGTGTGACAGCTACGGTGTTCAT
AACTCTTTTAAACCGAATAAAGATTCACAGGGAAGACAGAGCAAAACGTACAGTATG
TGACCGTTTAAACCGAATAAAGATTCACAGGGAAGACAGAGCAAAACGTACAGTATG
AAGCAACCTCTTATATTGTAATGAGAGTACAGCGTCCATTTGGCAGCTTATCTTAC
CAGCAGACCTTGATATCCAAAGAACTCCCAATAAATTTATTAAGTTCAATCATCAAAA
TCAATAGATGTGATATCCACACATCCCATGTAAGATTTAAAGAAAGCGGTTAGATATA
TCTCCAGATTTACTGATGATATTAAAGCAGGGAGGAATTTCTGGCAAAAGTTGTTCCCG
TCTTGAATAATA

>YNL134C, 376 aa (SEQ ID NO 332)

[illegible]

>YNR002C, 1349 bp, CDS: 501-1349 (SEQ ID NO 339)

SINK00ZC, 1349 DP, CDS: 261 287-1349
ATGCACAATTGAAGTCTTGACTACCCCTATCTCACACTAGTAGTAATTCATGTATC
ATTGCTATTGTAGTAGATAGAGAAGCAATACAGGAAGCTGACTTCTTCCAATCACC

88/251

ACGGCTGAATGCTTTTGTGACCAATTACGGAGCGCTTAAGAGCGGACGCGCTGGAACGG
CTCCATCTCTAAATCGGGGAGGAGAACTCCGATACACCGGACATGGCAATATAGTGA
CAGTAGATGCTACACGCCCCCAATAATTTTCACAGTAGATCATCAACAGTCTCTCTCATTT
TCGGAAATACAGCAACTCTCCGAGGATTTAACTCTCAAGCAGTTAGCTCCGGAAC
AGCGGTGATCATCTTTGAAACGAAATATATAAAGCAGGAGAACTGCTCTACCTAGAG
CTAGAATAGCCATCACTAACTATGTAACATTTCTACAGATCAATCAAAAACAATCTCAAT
CACAGAAAAAATAAAGGCATCTGACAGAGAACAAAGCAGCGGCAACACCCCTTTTG
AGAACCTTAGGCACTCGATTTCTCCGAGGAGTTCATCTCTGAAACAACGATCAGA
GGCCCACTCGCAAGATCATATGCAAAATATATCTCGGGGCAAAACAACGAGTATA
TGTACATCTGCGCGCTCAAAAATTTTCAAGGATGATTTGTTCGAGGCAATTCGGTGTACTC
TGAATCCGGTTTAGCCCCCGCGGAGTCCATAATTCGCAATCTCTGCTCCACTAGAC
TTCTCGGTTTTCCTCTACTAGTTCTTACATGTCATTCATCAAGAGCGCAAGGCA
TCTACTATCCCTAATGTTGTTGGTGTGGTGCATGTTTACGGTGGCTCGTTCACCTCA
TTGCTGTATTTTGGAAATCGCTTAGAGAACATTTTCGGTGTGACAGCCCTGTGTTCT
TCGGCGTTTGTGTTAGCTTCGGTGTCTATATACATCCCTTGGTTTGGAAATCTAGATG
CCTATAAGGACAAGGAATCCGACCTTGAAATGCGCTAGGGTTTATCTCTAGGATGGG
CACTCTTCACTTCGGTCTTCGCTGCAACCATGAAATCAACTATAATGTTTTCCT
TATCTTCTCTTAGCAGTACCTTCTTACTTCTATCCATTCGAAATCTCACAGCGGAAG
TTGGCGTCACTAGAGCTGGTGGTCTTGTGTGATAGTAGCCTTCATTCGCCGTGAC
ACGCTTACGAGGTATTCGCAACAGACAAAACTCGTACATATATGTTCCATCCCATTCGAT
TACCTAGCAATGATAAGGTGTTCTCTTAA

>YNR002C, 282 aa (SEQ ID NO 340)

MSDRQSSGNATFNPALDSSEGEFTSENDDSRHSOESICKIYTAGKNKNEYIYIGRQK
FLRDDLEAPFGGTLNPLGAPAVNKHFNAPALPLSGFALTTFVLWSPNRAQGITIPNVV
VCGMEYGLVQLIAGIWEIALENTFGTALCSFGGFWSFGAIYIPWFGILDAYKDKES
DLGNALGYLLGHALFTFGLSVCTWKSIMFFALFFLLATFFLLLSIANFTGEVGVTRAG
GVLGIVAFIAWNAVAGIATRONSYIMVHPFALPSNDKVF

>YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGACTGTTATGTGACTCTTGTGAAGNAGAGATACATCTTGTGTTCTAT
GTGAAGACCATTAAGAAACCTACCACTGTCATCTCCCTCTGGACACGAAGGTCACT
TCCAGTGACATCAAGAATGTTTCTCGATGAGATGAACAAGATGTCGCCGGCGTGGC
CCGGTGTGCAITCATCTAGTCTTCCACATTAATGATATGTTTAAACATATCATCACCAT
GTTTAGTTAAATCGTTTAGAGTAATATTACCGTCAAAAAGTCGGGTAAATTTTATTA
CCCTCTCCGAAAAAGAAATTTTTCGTCTCAATAGAGTTTAAATGCAATACCTGATATA
GTGTTAGTGTCTGAGTACTTCTTAGAGGATTTACGAAAAATAAAGCAATTTTGTCTGAA
AACTAGTAAAGGAGAAAAATGCTCGTTGAAGAGTTAGCAAGAGTTTGAAGAAAACG
TTTCACTCGATGATACCACTACTCCAAAGACTGTTTAAAGTGACAGTGTCACTTCG
ATGTCAGCACCCATTGAACACCAATGAGCTTTTATGTTACAAAGCCAGCCCTCGATA
AATCTAGTGTGTGTCTGATCTATATACGTCCGCTCACTTCAATCCAACTGTGGAAGAT
TTTGGCTATCATTTCAAAATTTCTTGAGCCACACGAACCTACCATTGAATCATGATACC
ACGCTCTCCGTAATAGGTAAGCACTGAATGGAGAGATGAAGCAATTTGAAAGGTGTA
AATGTTCTTCCAACTTAGGAAAAAGTGTGATATGATGAATTTATGCTAAGAACTT
TACTAGCAGTTATTTGGAACAATGATGAAGACGACTCCCAAAATTAACGGTGTCTTT
TAAGCATTAAGAAAGGTGTGACAAATTTGCTTATGGAATAATCTGAAGACAAAGAAC
CACTATTGAGAAATTTGGTGAATTAAGCAAGTTTAAATTTAAATTTAAACGATGACGGCAT
TCGAATTTCTTCCACATTCACGTGCCAATGTTAGACACACCTCAACCATCATCACCTTGT
AA

>YOL139C, 213 aa (SEQ ID NO 348)

HSVEVSKFEEVSVDDTATPKTVLSDSHFDVKNPLNTKWLNTKPAVDKSESWSID
LILPVTFSQVEEFVFIQNIPEPHELPLKSDYHVRNDRPEWEDEANAKGKWSQLR
KGADIDELWLRLTLLAVIGETIDEDDSINGVLSIRKGNKFPALWTKSEDKPELLRIG
KPKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

89/251

>YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)
TGTCTTACATATTTGCAATGATATGCTTGGTGATGATCTTCTCGGCTTTAGATATTTG
AAACTTAACTCTTGTCAACAACTTCCTCTATGAGTGTATAGAAATGTAAGTTATTAACAC
CGCGCAATATCGGCGAGCACTTTCGGGGAAGAACAAAGGAAGGCGCTTTTCTTCTCC
TCATTGCTATAGCAAGGTCAATTTCCGCTTCTCAGAAAGGGGTAGAAATCAATCTAGACGGC
AGATTGCAAAACGGCTTAAATATGCTATACGGCATTCACCGTGTGACGAATCGCA
CACCGTGTCTCTTAAATTTCCCTAGAGTAGAAACCGAGCTTTTCAGGAAAAAGACTACGGC
AGTAAAGAAATGCTTTTCTGCGCTATATAAACCGGAGAAATCAAGACATTTCTATGACTTT
GATTCAGGATAGAGCTTAAATGAGTGCATCTTAGCAAGCTTAAATTTGGACAGCTTCAT
TACTAAATTAAGATAGAAAAATGCTGCTACTTTTACATGATTTCTAGAAAACTCTTCTC
TAAATCTGGAGCCCAATCCCTCAATAGGTTTAGGTACGTGGCAGTGCAGAAAGAGAACG
ATGCTTATAGGCTGTTTAAACCGCTTTGAAGATGGCTACCGCACATTTGATCTGCTG
CTATTACCTTAATAGAGCAAGCTCGGTCAAGCCATCAAGATTCAGGTGTTCTCTCGG
AAGAAATCTTTGTTTACAAAGTATGTTGTACACAAACACCAACCAACCAAGAACTGAGG
TGATCAATCACTAAGAGGTTAGGATTTGGACTAGGTAGACTTATATTTGATGCTATGGC
CTGCCAGATTAGATCCAGCTTACATCAAAAATGAAGACATCTTTGAGTGTGCCAACAAAGA
AGATGGTCTCTCGTAGTGATATCAACATTTGGAATTTTCATCAAAAACCTGGGAATTA
TCGAGGAACCTACCAAGACTGGTAAACTAAGCGCTTGGAGTCTCCAACCTTTCTATAA
ATPACTGAAAGATCTATTAGATCTCAAGGTATAAGCTTTAGCCAGCTGCTTAACCAAG
TCGAAATACATCTTACTTCTCAAGACGAATTTGATTAATTTTGTAAAGATAAGGCA
TTGTGTTGAAAGTTATCTCTCGTTAGGTAGTACCGATCGTCCACTATTGGAAGAACCGG
TTTATCTTGAATTTGCAAGAAAAATTAACGTTCAACCGGACACAGTGTGTTATTAGCTGGC
ACGTCCAAAGAGGTTATGTTGTTGCCAAAAATCTGTAATCCCGATCGAATCAAAACGA
ACAGGAAAAATATTACTTCTACTAGGACTTTGAAGCTATCAATAACATATCGAAGG
AAAAAGCGCAAAAAAGGTTGTACATCCAAATGGTCTCTCTTCGAAATATTCAAGTAA

>YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSKILSLNTCAQIPQIGLGTWQSKENDAYKAVLTALKDGVRHIDTAAIYRNE
QVQGAJKDSGPREELIVTKLWCTQHEPEVALDQSLKRLGLDYYVDLYLWHPARLDPA
YTKNEDILSVPTKKDGSRAVIDITWNNFKTWELMQELPKTKTAVGVSNFSINLKDLL
ASQGNKLTPAANQVEIHLPLQDELINPKSKGIVVEAYSPIGSTDAPLKEPVILLEAK
KNVOPGHVVISHWQRYVYVLPKSVNPDRIKTNRIPTLSTEDFEAINNISKEKEKRV
VHPNWSPFVEFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2 :
723-1090 (SEQ ID NO 357)

AGGAGAGAGGCTGCTGTTGACGACGAGAGGATGATAATGAGGAAGAAGAAGAAG
AGGACCGGATGAAGAGAACGCTCTCGTCTAAGAAAATTTAAAAAGAGAGGAGACGCAA
TGTACAGAGAAGAGGAGAAAGAAAGATAGGAGCGAGACAAAGAAAGAGGGTTG
CGGTATCGAGGACGACGAGGATAGAGGAGCTTACTTTGTTTATATATATTT
AGTATGTAACAATCGCAAGAAATGGAGTGATGACATGTTGTAGTATTTAGTATGAGGTTA
CTGTGTGGAGGTTTACCATGATTTTGGCGAGAACACGCCATGAAATGCTCTTTGTACG
AAACTATTACCCCATTAATATTTTTTTTCTTTTAAAGCTCAGTTGACCTTTCTCAT
TCCCTTTCTTAAAAACAATGATCTGTGATAAGAAAGATATAATACATACACAAATAAA
CCCACTACGATCGCAAAATTAATGTTCTTGGCAAGGTAATGTAAGCAGCAATATCAATTTG
TTTAAAGAAATAGTTCGGAGGTAGCTTGTGTGACATGTTTTCGCAATGCCCCGATTT
TTGTGATCGCGGTAAATTTCAAGATTAACCACTCAGAGTAAATTTACTAACTGGAATATC
AAAAACATATGAAATTTTCAACATGAAATTTCTTCCGTTTTTTTCTCTACTTTTAAAC
AGCATACATGATAACTTAATAGGAACCGGTAAAGTGCACAAAAGCTGTCTACTCTCGAG
ACGAGTGCAGCTTGTGGCTACTTCTGTGGCTATCTTTTGCACAAACGAAATTTGG
TGAAATTTTCAAGGCTTCGACAAATCCAGCTGGTTTGCAGAAAGCAATGTTTGCATATCA
AGGCCAAAAGTTTCACTGTGTGTGAGAGCTGACATAGAGTATCTACGGTAGACATGATGC
TGAGGCTGTTTGTGTGAAGAACTAAGCAACCTGTTATTTATTTGCTCATTTATCCACCAC
CGTACAAAGCGGTGAGGCCCAAGATTGTCGCAATTTGGCGCAATTTGGCTGACTACTTGAATGGTGT
TCAATACTAA

92/251

AACTGCTAGTACTATGATGATGCTTTTCCTCTATTAACAACGCGCAAGA
TATAAGGAATAGTTCGGCAAGTTTTCAAAGATTTCCAAAGACAATCCAT
ACAGAACTGAAACCGCTTCAAAATTCCTGAACCGAGTTGCGAGGATATCT
GTATACCCCGTTCAAGTCAAGAGCTAGACAATGACGATACGCCGTCT
TACATAGGGCTGTATCTCTTCTGCTGGAGCTGAAGAGTCGGATCCAAA
TGTAGAGATCTTGGCTTAAGGTCCTTCTTAACGAATGTAAGTACGCCGA
GGTTTGTGGAATCAATGAGCTAATATGAGCGCTCCACGGGACCTCTCC
AACCTCAATGTATGACACAGATGATTTACAGGCTCTCGCAAAATCGCAT
CGCTTTGTGCGCTTCTGCTTAACCATATCAATTTCTCTGCCACTTACG
AAGACGAGTCACTTGGCCACTTGGGAACCTGTGGAATACCGTGGCGAAA
CAATGCGAATATCATCTCTTCTGACTCTCTTGGCTTTTCCCAAAAC
CAGGACTCTCTGATGCTGCTGAATAGATGTTAGCCGAACCGCTCTGCT
GTCTTTTGTGATCTTCATCCACTTTTGCAGTAATCAGTACGATGATTCCT
GTTTATCAAGTTTAAACAGAAATTTGATTTTAAAGTTTCAAAAGTTAA
TGGAGATTCACAAATTTTGGGTAAATATGCGTGATATTTGCAATGGA
TGGAGAAATGCGCAATATGTTAAGGCGGAGATCTGCTATTTGGAA
TATATAAAGTACTTATTTGAAGAGGCGACAAAGTATTAATTTCCAAATAG
TAATACCAATTTTGTCTCCAGAGGACTCTCGGATATGCGCCCTCTGA
AACCTCATTCAGATAATTTATTAATTTCCACATATTTGACTTTTGAATA
GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAAGCGGCTTCA
AGATCTTGTCTCTGAGCGAGTGCCAGAGACCGTTGGTGATCTCTAGTAG
CCGTTGCGGAAGAGGACTTTAGTGATGCGAATCTTTAAGATAATATCA
ATGTTGTTTATGATAGTAGAGTTTCTTAAATTTGCCATTTGAATAATATC
ACAGGATATCTGATCTTGCAGAAAGAAATTTCTGCTTGGGATAATA
GAGTGAATTAATCAAGAGGATGACCAATGGCAATCAACGAGCGG
TCGGAAGAGGATTCAGATAGATCTGTGCTAAGTGAATCACTGCTGGGTT
GTTCTGCTGCAATGAATATACAGAAATCTCTCTGCTATTTGAATAAT
ATCATTTCCCAATGACAAATTTTCATACCGAGGTCTACTCTTCATAC
ATAGACCAATTTGTGACATTAATTTACCAAAATCTCAAAACAA
TGCTCTTTGGAGCGGCTGGATAGTCCATAGAGTCCATCTATGATAT
TATCTCAAGGTAAATGAATGTGGGCTGAGCATCCCATGGCCCA
AAAGATCTGCTCCAGAGCAAGATGATTTACAGTTGAATTTCTCAAG
TCTATTAATGCTTCAAGATAAAGACCGCGGAATCCATGGCTTTA
TCGGATTTCTCGGCAACTTATATAACATATATTTCTGTCTCACTTTG
CCCAATGACAGCACGCTGCTTTAAATTTAGCGGAAGAACTGATGAA
TACCAGACGAGAGAAATCTAATCAAGAAATGTGACCATACACCAATA
TGACCTGTGCTCTCAATATCTTTCTGCTGATGCTTGAAGCAACCAATATCTTT
ATAGATGACTCCGAACTTTCTGCTGATGCTCTCGGATACATCCGATAC
AGAACAAAAGTTTGTGATAGATGCTTTTGGAGAGTTTCATATACCTTA
TGTTGCTCAATTACACTTCGCGGTAACTGCTGCAAGCATGACTATTCG
AGGTCTATAGTTACAGATGACACTTAAACTTTAGCCCAATAATCGACATTA
TTCAGGCACTACCAATCAAAAGCTAGATAATCAAAATGATCTTTGACCAAG
ACATTTAAAACGAAGAGACAGGATTTCTTATCAATCTAGAAACTGGT
TGGCAAGCGTCAAGATATTCAGGACTCAGCGAAACCGCCAAACCGGA
CCATTTAGATTTCTATCAATAGCTATGTTGATCTCAAAATCTACTAAG
CGCTTGAACCTCTAAGCAATGCGAAGTCCAGAGACCTTCGAGGAAGAT
GTTCAGAAAGTCTGATGATGATCAAGATAGTGTTTCCACGCTACATAA
TGCTGTGCGCAGAGCCCTTTTCCCTGCTCTGTGA

YBR133C, 827 aa (SEQ ID NO 54)

MHSNVFVGKPGFNHKKQHSKRFLNVSHPSPFVSNVYVLLPTTPR
YKEIVGVQVFKDFQRQSQIQNWKPLQIPEPQLQDICIPIPFNVKLLDNDTPS
YIGLLSWMLESRDNPVRDGLKVLNLECKYARFVGNKLILAPPRDLS
NLQLYQMIIYRLQLNRIVFAAPALITISLPLXEDSDPLATWELWTVRK
QCEYHPSLTISLALPRTPYSLVNLWLAEPVSCILLVSSIFASNQYDYP
VLHKFNQNLILKFKQVNGDSQILGNELCVILHGMKEYANNVKGESAYLE

93/251

YINLYLKKGDKVLNSNSHQFLQEDSRIMPPLKPHSDNLNLNLTSTLTPEK
DLVKYDLYESAILEALQDLAPRASAKRPLVLIVAGAGRGPLVDRTEKLIIS
MLFMDSKVSIIEKNQPAYLYLQKRNFDWMDNRVKLIKEDMTWKQINEP
SEKRIQIDLICISELLSGFCNELSPECLWSIEKYHSHNDTIPIPRSYSSY
IAPISPLFYQKLSQTNRSLEAPWIVHRPYCIISSRVNEVWRPHEPMAQ
KDTVQDEDDPTVEFSQSLSNEFKIKHRGEIHGPIGFPFSANLYNNILPSTL
PNDSTVRLKPSSEETLMNTRREENLIKCKDHTPNMTWSPIIPPLKQPISF
IDDSLSVLMSRLHSDTEQKVWYBWSLESFYLYMLSNYTSVATAASWTIP
RSIVQDTHGLSETAKPDHLDLSINKPMFDLKSTKALEPSELPRHEDLEED
VPEVHVRVKTSTVSLHNVCGRAPSLPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)
AAAGGCAAGTATGCGATCGCTAGAAATCTTTTCGGAAAACTTGAAGCAT
ATCATATAATTTGATGAACCTTGTCTTCAAAAGATGTTTACCAATATTTCA
ACAGATATGTGAGCTTCTATTTCTATTGACGCTAAGAAAGGCTATCACGT
GTGGGGGAGAGCTCAGCCACATTTGCACTACTTTTCGAAACCGCGTAGTC
GGAAACGACATTCCTCCGCTACCAAAACAAACGAAAGGACGTGAAAGGTAA
ATGAATAACATGCGACTATAAATTTGGCAGAAACGAAAAAAGGAA
AAAGAAACTGAAAACATATACGCTTCCCTTTAGGATACTTTCTGATTTACAT
CGTAAGATTTGGGTGCGTCAATTAAGGCAATTTCTCGCTCTATATCAACGA
CTTTACTGCTGCTCTTAAAGAAACAAATTTCTTTTACTGAAATTTCAACAA
AGTTTAACTCGAGGTGACCGGAGGCCACTGTATAATATAAANAATAGAAAG
ATGAGTCTCGAAGAAATACCTTAGGCAAAAGGGCCAAATCTTTTCTCTCT
GTATATTCGGTAAATCAGTACTCTTAAACGAATGGAGGACGAGCTCAATA
TGAAACCAAGTGATATAATTTAAAGTACTTACTGATGATGGGAGTACAAAT
GACGGCTGGTATTTATGGGCGCAATTTGAGAACCAAGAGGAAAGGTTTATA
CCCAGCGTATTTACCAAAAGATAGCAATAGAAAAACCAAGAGAACCTGC
ACAAATGATTTCTCGAGTACATAGGTAAAGTCTCTCTCGCATCAACAGGA
GAAAGATATACATTTGAAGAGTACATAGCGATATAGACAAAGCCCT
TGGAGAGCTTAAGAAGTGTTCAGTTGAACAAAGAGGTATCAAAATCGCCC
ACACGCTGCTCGAAGTTAGCACTCCACAGTTCGAAGATGAACAGACTTT
TTTTAGCACAGCGGATTTAAACTTAAAGTTCTGAAATCTTTTGAAGATATA
AGTAAGTCAAAATATCAACAAATCCCTAGAACCGAGTTCGGAAATCAGT
TCGCTAAATTAGATTTGAAATTTGGCTAAATTTGATTCGTCTCAAAATAACTG
CTGATTTACTTTTACCTTTGGATTTTGATCAATCCACTTTGCAATTAATTC
AAAGACATCAAGTCTCCGAAAAATACTACTGGAATTAGAACTGGAACA
CCTAAAGAAATTTGAAATAAAATCTTTTGGTATAGATTTTCAGATATTCA
AAGAAATAAGGAACATCAAGTCTGCAATTTGATTCGTCTCAAAATAACTG
GACGCGACTACTCTACCTTTGCTTTTGAACCAACCAACTGCCCCAATAAT
GCCTGAGCCACTGTAATAGAGAGCAATCCAAACCAAAATTTCTCTCCA
AGTGTAAACAAGTTTCAAGTGAAGCTCTGATAGAAATCATCTCTCGGTC
ACCACAGAAATTTGCAAGACAGCTCGGTGTTGTTAATCCCAATTTTAA
ACTTCACGACCCAGATCTGAGCAGATCTAGATATGACAGAGTTCCTAAAT
TGTTTGTCTGATAAAGATTTTTCGAATCCCGGGAAGGGCTCCAAACCA
CCATCATATCCCAAGTCCAGTTCAACCTCCACAACTCGCCCTCTTTTAAATA
CAGGTACACAAATAATAACCGAAGTTTCTCTCTCAAAACAAATATCCAC
CTAAAAACGAAGAACCAACCAAGTTTATTTCAATGGGCTAAATTTCCAAATCT
TCGACATCTTCCGATTAATCAACGGGCAAGTTCAAAATCTCTGCGCATGAA
TGGTCATGACTCGAACTCTAGGAAACAAACACTGACATCTGCTACTATAC
CTTCTATTAAACCGGTTAACCATGAATCTCTTACCCGCAATTTCCAAAT
ATATCTTCAAAATGCTACTCTCATCATCCGGAACAGAAATTCGCTGTGTTA
CAATAACCAATAAGAGGACGGAATCCGGAAGCTCATTTGTGATTTGTTC
ACAGGATTTTCAATGCTATCGCCACTCAAGTCAAGTTTCGACGCAAGAGAA

94/251

ACGAACAACCTTCAAAAAGCTAGACAGAGCTTTTGAATCAGCAGCAG
AAAGTCCTTACGAGCATTCGAAGATGACCTTCATTTCTGAAATGAGAA
AGCATAGAGAAACTCTTCTATTAATCTTTTCTTCTGAAATGAGCAG
TCTAATCCACAGTCACCAACAACTTTCATCTATCGATCCCGAAA
GATGATCTCCCATCTCTGTTCTCAGTGAATTCATTCGATGCAAGAT
CAGATCTTACCTCCATAGTAGAAGAACATCTGATTTACAGCCCTTG
AAAATCTCTTAAGCCCTTAATTAATCCAAATCCAAATTCGTTAGTCA
TAGGAATCTCTAGTAGTAGTAATATAGAGGAGTATCACAACCAA
GTGAGGGAAGACACAGACACAGACAGACAAAGACAGCAACAAAC
AAGAACAATGACCAAAAGATCATTTTGAAGAAAGCAAGAAATCTAAA
ATTATTTAGTAGACCTAACAAATCTTACCAATGATATCTTCCAGG
GATCTCCAGTAGCTTACCCAAATCTTCCGAGAAAGATATAGCTC
TCGAATGCTAAAAAGCAACAAATCTGCTTTTACGAAATGATATAGCTC
TATCAGAGAAAGAAATCTATGCAAACTGCGAATCTGTTAGAGCTGATG
GCAAAAGAGTACCGGCTCTATGAGGACTTGAAACAAAGCTTTTTCACA
CTTCATGGAACAAGCTTTCTTATTTTACGAATACAAATGATGAGAGAG
CGCTGAGCTGATGATATTAACGAGACATAGGCTCTTACCTGCACTGATG
ATGATAGGCTCATTTCTTATACCTGAGCTTGAAGAAAGGAGTAACTC
TCTTTCAATTTGGTCCCTCCGAAACGGGGTCAAAAGGGCTTAACCTT
TACGAAACCTCGGCTCATTAATTTTGAAGTTGAGATTAATCTGAAATGA
AGCATGAGCTGTACGCAATTAAGGCACTATGATATGATGATACAGC
GTCCCTGATATGATTCATATGACACACAAAGATCTCTTACAGAGAGC
ACAGACGCTATTTGGAAGATGATTAACCAACCACTTACAGATGATGCTG
AAGAGAGAGGGAAGATCAATTTGATGAGGATGACACCCAAATATAA
AGAAATTTCTAATTTCAATGCAATGCAACAGATCAATTTGACACGAGATTA
CCTGGAAGTTCAGCATTTGAATACCTGCTGAGCAGACTTTGA

YBI085W, 980 aa (SEQ ID NO 32)

MSLEGMTLKGAKSPFLIAVNOYSKRMEDELNMRGDKIKVITDDEYN
DMWYIGNLTKKEBGLYPAVTTKRAIKREPM.LHKSPTQESGNSGYKGN
LNDASNIUKVSSHQENRYTSLKSTMSIDKALELRSGVBEVSKSP
TRVPEVSTPQLQDEQTLIQEKTRNENTHDSLFSTADNLNSESILKNI
SKENISTKLEPSSSEVRQLDKMKSWSPEEVTDFSLVGPDSQCNK
KEHQVSKLLELEHLKELEINFGIRFOJFKEIRNIKSAIDSSSNKL
DAVSTPAFENQAO.LMPAATVNDEIQQOISCKNKLSESSDRKSSSV
TTBELQRPSSVVNVNPKLHDPAEQLDMTEVPM.LFADKDFESRPAKPK
PSYSPVQPPQSPFNNRYTNNNARPPQRYTPPKKNKPTVYNGLLPNS
STSSDNSTGRKFPAMNGHDSNRKTLTSATIPSIINTVNTDLSLPAISN
ISSNATSHHPNNNSVYNNHKTSGSSFYDLFNRI.SMLSPKSSPDEBE
TKQPSKASRAVFDASARRSSYGHSDASLSEMKHRRNSSILSFFSSKSO
SNPSPPTQPTFLIDPAKMTSHSRQSNYSHASQSYSHSRKSLVYSP.L
KTSLSPIKSNKINIALAHSEPTSSNNKEAVSOPSEGRHKHKKHRSKHKH
KNSSSKDSSSEKSKKLFSTYESFVSGKEFRSPSELQKSTKSLLEPR
SNAKQOQSAPTEGRISITAKESMOTADCSGMSKSGTGAMTWKQRPFT
LHGRLSYFTNTDEXERGLIDITAHVLPASDDRLISLYA.SLQKXY
CFKLVPPQPGSKKGLFTEPRVHVFAVENSSEKMLSAIKATIDIDS
VPIVSSVATPTIPLSKAQTLEEARLQTL.RDAEEEBRDQPMDDDTQNK
RNSNVPIDQGFETSDYLESSAFEYPPGR.L

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTATATTGGCTTTTTCGAGAGCGAAGAGTGTAGGCTAGCGC
AGCGTAAAGCTAGTCCATATTTAAAGTATCAAGAAATATCCAGGAAG
CGGTGAGCAACGACAGAAATCCGTGTTCTCTCGATACAGCATAGTAGT
AAGATACGTGCACATGGAATGGAATAACGAAAGTACGATCAGACTACT
TTATTTTTCAGGCGCGGAATCAAGCGATGATGACATCTCTGTTT
TCTATGTTGGACAGACAGTCCGTTATCTTAGTGAGATTTCTTATTAAC

95/251

GAAATTTCTTTCGCTGCTGTGAGATTGCACTGCAATAGCGCAGATTCT
GCTTCTTCTCAATAGAGTACTTAATTAATACATTTAGATGATGATTA
GACGGAAGCTGCAATCTTTTGTATATTTAGATGATTTCTTGTCAAAA
AGCATTAACATCAACATACATTTGTATTTTGAAGTACTTACAAATTA
ATGAAAGTTTCCGATAGGCGGTAACTTTGAAAAGCAAACTTTGACAGATT
TAGAGTGGCTCTAAATPAACAAAAGCATGTGTATGTCCTCTCAATTA
CTTTATTTGAATGATCCCAAGGAATGCGGTCAATCTACAGAACGAA
AAGTCTGGCCTAATCAAAAGGTAAATTTGAAATTCGATGCTCGGAAAAATG
GAAAAGGCTTTTGAATAAAATTTGTCATTTCCGTATGCTCGGAAAAATG
TACAAAAGTCCGACATTTGTGTGAAGCAACCAAGATTTTCCAGGCGGA
CCATCTCTTCAAGTATCTTATTTCCAGAAATCAACTTCAATGCTCTA
CAGTTTCTTCAAGTATCTTGAATTTCAATTAAGATGATGATGATTA
CCCTTCTCTTTTATCTTCAACAGAGATTAATTAAGATGATGATGATTA
CGTGTCCGAAAGCTGTACGAAATAGCAGTGCAGACGCGCAACGACAG
CTTACAGATGCGTACTTACGATTTGTTTCTTGGCGCACCAATGATTA
GGAGTCTCAGAAAAGCACATTAAGAAATAGGTTACATTTTGGCACCC
TACATGTTCTTGTATCTACAGTATAGCTATGCAATTTTCTTGTGATTA
CCAGCAAGTTTACCTGGCAAAAGAAAGTGCACACAGCGGCTGAAGC
GTGATCTATGCTCCACGTAAACCAATTTGAATTAAGTATTTTCAAGATA
TGTACAGATATGATGACAAATAAGACCATTTGGTGTATTTTGTGATAT
TATCTTGGAGCATATGCGCTCAATTTGGGGCGGGTCCCGGTGGCGG
CTGGTACGAAAGAGATGATCTATTAACAAATGAAGATCCATTTATCC
TCTGTGACAGCATGCTGTGAAGTATGTAAGTGTGATATTTTGTGATAT
TCCAGGAAGCTCAGAAAAACATGATGCTGTAAGTGTGATATTTGATG
CGTTTGTGCTTGTCTGCAAGGATTTAGATATTTATGATGATGACACCA
GGCTGTGCAATGTGAATAATGATCAAAATTTCTGTACACAGATGAGCA
GGAAACACGCTGAGAACTCTTAAGAAATTTTATTCGAGATATGTCGGG
ATGATATACATGATGTGAAACCTTTTAAATTCGAGATATGTCGGG
TTTTACTTTGCAATGCAAGGCTCAGTTCGATTAACCTTTGGGAGATTTGA
CACTGCTTTTATATGCTTACAGTGTGATATTTGCAAGCTATTTGAC
GTAATCGAAGATTTTGTACAGAGCCAAAGGAGAAATTTGACAGTAT
CTGAAAAAGATTTTCTTCAATATGATACCTGTTAAATATGCTGTAAT
TGTGCTGCCAAGTTGAGAGATACATAAATAATGACCCGCTCTTA
AAAAATAAAGTCACTGTGCAATGAGAGTACCTTACCTTATCAGAGCTTCACT
AATGCTCAATTTGCTGTAGATACCTTACCTTATCAGAGTATGATGAT
ACTGCTTTTGGCGGCTCCAGGCAACGTAATGCTGATGATGATGATGAT
GACGATCCACTGTACACTGATTAACAACAAGACGTTATGCGAGCT
GACTTTAAGAGCTTGAACGATCACTTACATTAAGTATTTTATTTTGT
CACTGTGCTAAGCAATATGCAATATGCTGCTTGTGATACAGTTATGACG
CTTTTATATGATATCTTGTGAATGATGAGATAGTTTGTATTTCTACATCTT
CAAGTAACAAATCGAAGATTTGAGATAGTTTGTATTTCTACATCTT
TCTGAATACCCGGAAGGCTGTGCTGTGATATGCAACTTGTTCGGCAGT
ACATGAGGGAATCTCCGAAAGATGACCTCAGAACTGAAATTTTCGGAG
ATGCGTCAGGGGTGATGCTGCTGAGAGCACTGCGATGATGAGATTA
TGAAGATATTTGTAAGATGTCGGGAGAGATGAACTCAATGCCAATCAT
TCAAACAAAGGCGAAATATTTACGTTGATCTTTTCTTCTGTTAACT
CGCTTCAATAGGCGAATATTTACGTTGATCTTTTCTTCTGTTAACT
AGTGTAGTGGAGCAACCGCACCTTATTTGAGAGAACAGCTTCCGAGG
CTGGAATCAATGTTAGGCTTGAAGGCACTCAATGTTCTATTTCTTA
GTACTCGGAATCGGAAGATGATGAGAGTGAAGAGCCCTCGAGACCCAA
CATATCAAAAATTTCAAGATGACGGAATGGAAGAGCCCTCGAGACCCAA
GATTAACAAAGATATCTCTGTCGAGGCGCAAACTTTTGGCAGCTCT
TGAATTCAGGACTTGCATCAGTTGCGCTTATATGATGATGATGATGATG
GCGACACACCTCTGTGAGAGTACAGGCGCCACCGGCTGTAAGGAGC
GAGATTAATTCATCTCCCTTGAATGACACTGCGCTTAAGGCGACGTGA
AATATGTCGTTCTCTGTTTACCTGATACAGGCTGCTGCTTATTTCTC
ATGATCAGGTTGAGCCGATGCGGTTGCTTGAATGTGGCCCTGTAAAGAA

96/251

CTTTATGAAAGAGTTCCGATGCGGTTACTGATTTATAGTGGGATCT
ACGATGATCTGCTAGCACTAATTTACAGACAGGATAGCTGCTGGGAG
AATATTGTTGAGTGACCTTTAGGACCAACAACGTAATAATTTGGTTACCT
CATGTAGATGAGTTTACAACTTTGAAACGAGGCTTACCGCGACTGCG
AATTTGGGGGACATTAACCTTTTGTAGCGCTTTTGAGAAGCAATC
TTTTTGGCGGCACAGCACTGAGCTGTAGCTGATGCTGCTGCGTGACGG
TATTTGGCTTACGGGACTGGCAAGAGTGATGGACATCAACAGGATCA
AAGGTCGGGAAGATCTACGACAGGTCTATCCAGCTATCAACACAGGATG
TTTAAATCTAATACAGGAATTCGAGGTGCTTTAGGGCATCTTATTA
TATTTGGAAGAACTGGAAATCACAGCCGCAAGACACTGAACCTCTTT
TACCCCTCTTTGAAATGAACAGGCTGGAAGCCATTTGATGTGCAAGC
ACAACCAAGAGTGAAGAAATTTGCCCTCTCTTGGAGAAAGTATTATTAG
GGTGTATGATGATACGGGAAGTGGGTCTGCGCAAGAAAGGTGCTGCGA
CAAGAGTTGTTGCTACTGACGAGTACGCGAGTTCTCATCGGAACGAAA
TTAGTCACTTAAGGAATTAACATTAAGCAATTAAGTATGATGATGATGCT
TGATATAGACTTATATATATTAGTCTATCTATCTAGAAAACACAGTTAGCGCA
GAGATGGGGCTCTGTTATCTATCTATCTAGAAAACACAGTTAGCGGCGCA
AGGAATCGTAAAGGTGAATTAACCACTTAAGGAAGGCTGTATAACCGA
ACAGGTACGCGAGTTCTATGAGCTTGAATCAAGAAAGGAAAGAGGCC
AGCATGTTGATGCTGCTGGCTCCAGGACAGACTGCTCTGCTGACAGTG
GAACTGATAGAAGAAAGGACAGATGCTGTAAGAAACAGCGGACAGCTTC
CATGTCGATCAATTTGGTTACGCTAGCTTCCAGGAGAGCAATAGCAGTG
ACAGGTGCGAAGATTTAGCAGAGTATGAGGACAGCAGCAGCTGATG
CATGGTAGTCTAATGCGAGTACCAATGCGACTACCAACTCCAGCACTAA
TGCTACTACCACTGAGCACTACCACTGAGGACTAGTCTACTACCACTG
CCAGCACTAAGCTCAGGACTAGTGGGATTAACCACTGAAGTACCACTCC
AGCACTAATGCTACTACCACTGAGCACTACCACTGAGGACTAGTCTAC
TACCACCTGCGAGCTACAGCTCAGGACTAGTGGGACTACCACTGAAGTA
CCAACCTCAACACTAGTCTACTACCACTGAGGAAAGTACCACTCAACACT
AGTCTACTACCACTGAGGAAAGTACCACTGAGGAAAGTACCACTGAGGAA
TGCTAGCACTCACTGAGCACTACCACTGAGGAAAGTACCACTGAGGAAAGT
CAGCACTAATGCACTACCACTGAGGAAAGTACCACTGAGGAAAGTACCACT
GAGCCCAATGAAGTGGCAATGCTGAGGATATAGATTTCCATGCTACAGTCA
CGACATTAACAAAGAGTCTGATAGCGGAAAGGAGTCAAAATGGTTTTG
TAGAGAGAAGAAAGTGAAGCAATTTCCCAATATCTCCGAGAAATATG
AATGCTTACAGTTCTTGGATTTGGCTGAGCAAAATTAACATCTTTT
CCTCTATGTTATGACGATATCTCTGCGGAGAGGAGTATTCACACAAAT
ACGGATTATGCAAGGGCTGTCAAAAGATGTTGCGAGCTGTGCTGTGTTGG
GCTGGCCAGAAAGTATGTTATGAGGAGTGGCTTGGGAAGCACTAGCTGT
CGAGAGAACTGCTGCGAAATGACGAGGAATACAAAGAACTTTGGAAGACA
TCGAGCCATATCATGAGGAGCTTCTGAGGATTTTGAATAATTTATGCGGTA
AAAAGGGGAGATCTACTCTCAGATACAGAGAAATTAATGCTTGGTACCT
GGCCATTTAGAGAGAGAGAAACATTTAGTGTATTTGGAATTCAGCAAGAG
GCAAGCAAGGAGCCAAAGTTTTCGCAATGCTGGAAGGAGATCAAGAG
TTGATTTATAAGAGTGGCAACTGCTGGAATTCGAGCAGAGGTGCT
CGAGTACTTTTGAATGCGGAGGAGAAAGTGGCGGGAGAAATGGGAGG
CAAAAGCAGATACGCTCTTTGGAAAGGCTGAGAAAGTGGAGTTT
CAGCGTTTGGTTCCATGACAGCGCTGACGTCAGCGGTCGCGAGTACGT
CAAGCTGCAATGAGGAGCATGACAGCTAGTGGCTGAGGAGCAGATATGAAT
TGAATGAGAAATGCACTTGGAGATCAGTGGCTGGGAGTTACCCCA
TCTAAGTGGCGATGAGGAGCATCTGCTGCTGATGCTGATGAGGCTGTT
CTCAATTAACAACTTTGGCAGAACTGGAATTAATCTTTTGGAGCAGATTT
CGGAGTGTGGTTTACCACTAGGCTTGAATTTGGCAAACTGTTGAAGTT
CTCGCTGAGATTAACAGAGGTACCGCTGTACATGCTGATGATGAGGTT
TCACAAAGAGCTGATGAGGATGATTTTCCAGCAGGATGATTTGATATAA
TATTACTATGATAGATTCGAGCAGAGAAAGTTGGAGAGTGA

97/251

YDR545W, 1796 aa (SEQ ID NO 138)
MKVSDRRKFEKANFDEFESALNNKNDLVHCPISITLFBESIPTEVRSPYEDB
KSGLTQVXFRTGAMDRKSFKEIVISVMGKNQKFLTFVEDEPDFQGG
PIPSKYLIPKINLWVYTLQVHTLKENRKDYDTLSLPYLRNGYINELSF
RVLERCHEIASIRPNDSTMTFTDFVSGAPFVRSQKSTIRKYGVNLAP
YNFLLLHVDLBSLIFSAYQASLPGEKKVDTEBLKRDLCPRKPIEIKYFSQI
CNDMMNKDRLGLDILHILRACALFVGAGPRGGAGDEEDRSITNEEPIIP
SVDEHGLVKLRSNPTRRLRKTLDLDAVKALLVSSCACTARDLDIFDDTN
GYAMWKIKILVHEVAQETTKDSYRITLVPSSDGI SVCGKLFKNREYVRG
FYFACKAQFDNLWGLNCCPYMPVTVDIASILLNRRVLPREPGRGIDEY
LENDSLQMPVRYREIVLPKLRDRTNKTAAAKNKVTVAIDELTVPLMW
MVHFAVGYPYRYPELQLLAFAGPQRNVVDDTTRRIQLYTDYNNKSSSEP
RLKTLDLGLTSDYVFYFVTLRQMQICALGNSYDAFNHDPMDVVGFEFDP
QVTNRDISRLVLSYMFNLTAQCLLVEYATFQYMRBELPKNAPOKLNPRE
MRQGLTAGRHCVGSRFETDLYESATSELMANHSVQTGRNIYGVDSFSLT
SVSGTTATLLQERASERWQLGLIESDYHCSFSSSTRNAEDVVAGENAASD
HDQKISRVRKRPREPKNSTNDILVAGQKLFSSFEFRDLHQLRLCHEIYN
ADTPSAVQAAPPQYKTELPFLPLIALASKGVKYVSFLVPYTVLLANC
MIRLSRCCGLNAPVRNFIEEGCDGVTDLVYGIYDDLASTNFTDRIAAWE
NIVECTFRNNVKLGYLIVDBFNHFEVYRQSQFGGTTNLDPDFDAPEKAI
FLSGTAPFAVADAALQRIGLTGLAKSMDINELARSEDLSRGLSSYPTRM
FNLIKESVPLGHVHKWKVESPQPEALKLLALFELIEPESKAIIVAS
TTNVEELACSWRKFRVVMIHGKGAEEKVSRTEKFPVTDGSMRVLIGTK
LVTEGIDIKQLMWIMLNDNLNLIIEILQGVGRUDGGGLCYLLSRKNSWAA
RNRKGLPPIKEGCTIEQVREFYGLESKGKGQHVCGCCSRTDLSADTV
ELIERMDRLAEKQATASMSIIALPSSFQESNSSDRCKYCSSDESDTCTI
HGSANASTNATNSNTNATTAASNVTATTTASINVRTSAITTESINS
STNATTAASNVTATTTASINVRTATTTESNTSNTSNTSNTSNTSNTSNT
SATTTESNTSNTSNTSNTSNTSNTSNTSNTSNTSNTSNTSNTSNTSNTSNT
DANKDGAEDNRFHPVTDINKESYKRGKQSVLLERKKLKAQFPNTSENM
NVLPQFGRSDEIKHLFDYVFCPEGVTFQYGLCKGCKQMFELCVCM
AGQKVSYRRMAWEALAVRMLRNDDEEYKEYLEDIEPYHGDVPVGLKYFSV
KRGEYLTQIRNYAWYLAITRRRETTISVLDSTRGKQSGQVFRMSGRQIKE
LYKXVMSNLRESKTEVLQYFLNWDKKCRSEWEAKDDTVFVEALEKVGVP
QLRHSMTSAGLQGPQYKIQFVSRHHRQLRSYLSLGMHLRDLQALGVTP
SKVPHWTAFLSMLIGLFYNTKPRQKLEYLEQISEVWLLPHWLDLANVEV
LAADNTRVPLVYMLWAVHKELDSDVDVDFRFDIILLCRDSSREYGE

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)
AGAGTTGTTGCCACACATAAGCCGCTTTGGAGTGTGTAACAAATCCGTC
CTTGGGTCTTCAATCAATGGCTTGGCGGTATCTCAAAAGAGCGCAAACT
AATAGCGCGCACATTCGACGCATTTATCCGGTGTCTATCGACTAGGGCG
AAGAGTCACGACCTATTTTCTTCGAGAAAAAAGTGTGACCTTTTCC
GTAGCTAGACGCTATCAGGCGCTCAGCAATGGAGGACACAGCGGAAAAA
CAATAACAAATGGTAAGCAATACCTTTTGGCGGTACATTCGCTATGAA
ATTGGTGAGTTAATCTAAGATAGTCTCTCTCAAAAGGGCCCATATAT
TCTCGACCTTGAGCGTATATAAGACTATTAACACTTGGTCTTCTTAGATAT
GGTGTCTCTCTCTATTAAGTTTTCAGGGAACAATATCAACACATATC
ATAACAGGTTCTCAAACTTTTGTGTTTAAATAATACTAGTAAACAAAGAA
ATGACAGTTCTTATCTAAATTCAAACAGAAATGTTGCATCATATTACAA
ATCAAAATTCAGCCCAAGAAAGACTCTAAAGAGAGATTTAGCGAAATCT
ACCCCATCTCATCTCAAGATGTAAAGCAATTCGTTAAAGACATGGCAAA
ACTAAATTTAGCGATGTTGATTAAGAACAGGTATATGTTGTTATGAGAGG
TATTTCCAGGGAGCGTATGGAAAGGTTCCGTTTGGACCCCAAGACGGTA
TCTGTTTTCAGAGGTGTCGATCGGACATTCAAAGAGACCTGCCCAAG
GCAAAAGGAGGCTCACACCACTACCAAGAGCTCTCTTTTGGTTATTGCT

98/251

MACTGCGAGGTTCCAACTCAAGCCAAAGTTGAAGAACTTATTCAGGATC
TATATGCAAGATCGAGACTACTAGTCATGTCGTTCAACTTTTGATTAAT
TTACCAAGAGCTTACACCCATAGCTCAATTCCTATTTGCAATCTG
CTTGAAAGGAGTCAAGATTGCTTAAGGCTTATGCTCAAGAAATTTCCA
AGCAAGTTTATTTGAGTTTACTTTTGAAGATCACTAGACTGCGGT
AAATGCGAGTTATGCGACTAAATTTATTCGTAATGTAATTCAGAAATG
CAAAATGGGTGAATGAGCCAAATGCGGATTTGCTGAGCTTGAATGAGACTTAT
ACTTATGTTGTTCAAGATGAAGATTTGCTGAGCTTGAATGAGACTTAT
TTACCACTTCACTTGGATTCAGAGAGTGTAAATGATTCAGCATCATC
CCATCTTGCGGCTCAGCATTCATTCACCTTATTCCTGCTGCTGCTG
CTTTGAACGGGTTGGCTGGCCACTTCAAGGGGCTTATCAAGAAATGA
CTTGAATGGTTATTTGCACTTAAAGAGATTAATGATGATCACTCTTA
AGATACGATCGAAAAATATTTATNGGATCTCTAACTCAGAGAGATCA
TTCCCGGTTATGCTGCTGCTGCTAAGAAAACTGATCTGCTGTTATG
GCTCAGGCTAAGTTGGCATGAGACATTTCCAGATTATGATGAAATTCAA
GTTAGTTTCATCAATATAGAGATGACACCTGGGCTTATGATGAGAAATG
GTAAACATTAATAATCCATGCGCAATGATGATCTCATCTGCTGCTTGA
TTACATATTTATGACTTAAAGAAATCTTCTTCTATACGCTTTATTTGG
CGTTCAAGGCGATTTGCTATCTGCTCAATGATCAGTATGATGAGGCA
TCGGTGTCTTCATTTGAAGGCCAAAGTCTTATTTCTACTGAGAAATACAG
GAATTTGTCAAAACATTTGAAGCAACATATAG

YCR005C, 460 aa (SEQ ID NO 72)

MTVPYLSNRNVAASYIQNSNSQEKTLKERSEYPIHAQDVQFVKHEGK
TKISDVLQYGVNGRIGPSVWEGSVLDEPDRFRGRTIADIQKDLPK
AKGSSQPLPEALFWLLTGEVPTQAVENLSADLMRSLESHVYOLLDD
LPKDHPMAQFSLAVTALBESSEKFAVAQGISKQDWSYTFEDSLDLG
KLPIVIAKIYRNVPKDGKGEVDPMADYAKNLVNLISKDEDPIDMLMY
LTIHSDHEGANSATSHLVGSALSPYLSLASELNGLAGPLGRANDEV
LEWLFALKEVNDYDYSKDTIEKYLMDLNSGRVIRGYGHAVALRTDPTM
AQRKAMDHFPELFLKLVSSIEVAPGLVLEHGTKNPWNVDASHVL
LOYGLKESSEFYTVLFGVSRAPGLAQLITDRAIGASIERPSYSTERYK
ELVKNIESKL

YOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCTCATACTTTCCGTTTGATCCCTACTTCTTACTTCCCTTTT
TTCTCTTTATTTGCTTGTGTTTACATTTGAATGCCATTTTACTAGACG
AATAGCTAGTCATTCGCTATCTCCGTTGTCATTTTTCATAATTTCT
CATCTATATAGCGAAGTACGAAAAAGATGTCATTGCCGGCATTCGGCC
TTCCCGGCCAANTGACTCATTCATCAGATCGGATCGCCCTTAAATCCGC
AATTTACTTTGCCCATTCGCGGAGCCGTTCTAAAGCCGCGCTGCTGC
CCCATATCTCCCTTATGATCCGGAGAGTCCGGTTTCTTCTTCTTGT
TAGTGCCATTTTGTGTTGCCCAAGTTGGGAAGTCCGATTTGACTTTAA
GGAATCTACGGAAGGATCTAGGTTCTTAAACAAATATACAGCGCGTG
CGATGATATATTAAGATTAAGATTTATGATATGATTAAGATTTAGTCTG
ANGATTTCTCTCTGATCTTTTCCGCTATATATTTTCTCCCTCTG
TATTAATTCGTACAGTCAAGATGTCAGAAATATAGTGTGCGAGCATAT
ACAAAGTTCAATACAAATATCAATAAAGTTATATGTAACATGCTCATCTA
GTTCACCATTCATAGAACAGATTCGTTAAATATGCCATTTTATGATGTC
TTCCCGGTGATTCGGGAGTCTGTTATGCTGCTTTGAAAGCTCAGATTGC
AATACCACTTTAAGAGAGCAACCGGAGGTTACCAATTCATTCATGCGCT
CTTTAGCATGTCACCAAGAACATCAAGGCTTACCGCGCATCTTGC
TTATATAGACACCCCATTTTCCGTGTCAGCCACCTCCGAGGAGTCA
TTGGAAGTCTGTTGATTAACGCTTCTATTTGTTGTCATTTCTGCAAGGTT
CCAAAGAAACCTGGCATGATCTGTATGACTTATTTAACTGATAGCTG
TATCATTTAGCCAGCTCGGTGATTTCTATTTGCAAGATGTTGATCTTTCCA

99/251

AGGCTTCGTTCTGTCATTTCCAACTCCCTGTATATTTCTTTAGTCCAGTG
ATGGTTTCTTAACATTTCTTAAGAACCATCTCTCACTGTAAGAAATTCGGCAT
TGAAGAAGAGATCATGGGTGTCACCAAGCTCAGATGTCAGAGCTTCCA
CTTTCATCGTAGATTAACATTTGATGTCAGGGCTATCTCTCGTTATAC
TCCATGCTGAGCTCCGTGTAATTTGGCGGCAATTCGGGAGACTATTTAT
TCCGTTGTTTTCAGAGTCAACTTCTCTATCGAGATTAATATGAGATCAAT
TGAATATTTATATCATATGATGATCAATACGATGATGATGAGTGTCAAG
GCCAAGAACGGTAAAGATGATGCTACCTTATGATGAGCCATGCGGGTGA
TAAGTGTGTTGCCAATTTGTTTCTTGTGTTATTTGGTACATTCAGCAGA
TTCATGGAACCTCATGTCATGCGCATTAAGATGCAAGCAATCTCCCAT
GCTCCTGGGCGAGATCAATTTATTTGCTCTGTGTGAGGCTGCAAGTACTT
TGCCATTCACCTTACATTTATCTACAAAGGCTGTTCTCATGTCGATTTG
ACATGCTTAATAGATGAACGATGAGAACGCAACCAATGTTGCCAAT
TGCCTCTCCAGTTAAAGAAATATTCGATTAAGGGCTTGGAAATTCGTTGC
ATCGAGATCTGCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MLLLILPFCIFYLPEFCINRWTSPEYSAADYKSSIOYHKSYSNMPHS
VPSIEDPSLKIALILGAAGIGQSLLLAQLOYLKESNRSVTHILA
LYDVNGEALNGVTAADSHIDTPISVSHSPAGIENCLHNASIVIPAGV
PRKPMTRDGLFNVNAIGIISQLDLSIAECDDLSKVFVLVINPWNVLVY
MISNLKHNHPQSNRSGIERRIMGVTKLIVASTFLREINLESGLEPRN
SMDPVFVIGHSGETIILPLFSQSNFLSLNEDQLKYLHRYQVGGDEVYK
ANNGKGSATLSMAHAGYKCVQFVSLGNIEQLHGTYYVPLKDMNFI
AAGAQQLPLVLDGADYFALPLITTTTKGVSYVDYDINVMNMEMRQMLPI
CVSQLKNIIDKGLFVASRSASS

YBR019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATGCGTTCGCTGATTTATTAATCCCGAAGAAATAGGCTAAAACTATCGC
ATTATGATCTTATGCTTATTTGATTTCTTATTTGAAGTTGTGTG
GGCCAGCTTACTGCCAATTTTCTCTCATACCAATGATTTGATTAAT
GTGAATCTTTATTTGTTGCGAGAGTGGCGCGCAGACATCTGCTTT
CAGAAACGGCAGCGGTGAAGACGAGACGACGAGGAGAGCTTCCGTC
GGAGGCTGTGCGCCGCTCGCGGCTTAAATCCGACTTCTTAATAGCA
ATGAGCAGTTAAGCGTATTAATCTGAAGTTCCAAAGATCAAGAGAGTTTGA
GCTPAAGTAAATGGGCTCTTTTACATTTTCCACAAACATATPAAGTAAGTTAG
ATATGATATGATATAGGTGCTTATGATGATGATGATGATATTAACCTT
ATATGCTCATCCAAAAAAGATTAAGATTTTGAATTTGAAATCAATATTA
ATACAGCTCAGTTACAAAGTGAAGTACTTCTTAATATTTGTTGTGTAC
AAGGTGTGCTGATTAATGTTGTACACACACTGTGTGAAGTATTAATGAT
ATGGAATAGCTGATGAGTCTTGAACACTGTGCAATTTCACTTAATGAT
TCTGTAGCCAGGTTAGAGTCTTGAACAGCATCACTCACTCTTATGAT
GCTTATTTGTTGACCGAAGAGTCTGAGAAAAAGTTTTCAAAAGATATATA
AAATGATTTGTTGATTTTCACTTGTGCTGTTTAAAGCTGATAGGTAATCT
ACCAAAATCCCGTGAATATCATCAATATCAATATGAACTGTGCT
TTTATTTAGTTAATGCAACAATACAAAGTTTCCAAATTTGTTTTCAT
CTTGTGCTACGCTATAGTATGCTACGAGATTTCCAAATATGATTTCT
ATCCCAAGAAATGCTCCCTTAGGCTTAAATTCGATTTTCAATAGCAGAAAAA
ATAGCCATGAGATATCTTGAATGATCTTTTCAATAGCAGAAAAA
TTGGGAAGTTTGTCTTCTGCTTATTTTAAATTTGAGGCTTATGATGCA
CTTGATTTAATCGGAGAGATCCGTAAGTATTCACAAATTTGTTGTGCT
ATATATGAGCTCAAGTATGTTGTGTTAGGCGGAGGAGCTTATCATCTTGC
GAGAGCTTATATGATTTCCAGAGATCATTTGCCGATCAAGGATATATCCAC
CTACATGATTTAGCAAAAGTATGATATTTGCAAGCCGTGAATACCTAGGAGC
GTACAAATGAATGAAGTTTGTGCTGATGATGAACTTGGGTTCCGGTA
AAGGTTTACAGTTTGTGAAGTTATATCATGATTTCTGCAAGCTTCTGCT

100/251

ATTGATCTTTCATCAAAAGTTHACGGCGAGAGCAGGATGATGTTTTCGA
CTTGTACGGCTTAAACACAGATPAGGCGCAAAACCGCAACTGTAATTCGCACACCG
AGTTCAGCGCTTGAAGACTCTCTCGAAGATTTATGGAATATGGAATCTACTGAG
AATCTCTTTGTTGTTACCACTTAAGGTTGTCGAGCGCAGATATTTCCGCTGCA
AGATATGCGTTATAGACGCAAGATTTTGTGTACTATTTGGTCCCGGCACACAGAT
TTCAACGACACAGTTTTCGCAATTTTGGCGCGCCAGCATTTGTGACTCTGAAAGTG
ACCGGACATAGCTTTCTTCTTCGCTATAGAAATATGAGGAAGAGTATATCTGA
TCCCGATAGTCGCTTTATATPAGCGCCACATACCGCATCGGAGAGTAGCTATCTGTA
TTTTCGAAGGGTTAAGTTTAGTTTATGCAACAAGAATCTATCAGTTTAAACGGTT
AATAACCGCGTTTAAATGCGCAATCATATAGTAGTATCTGCGTTCTTTCCACAGAAA
CCGAGTTTATCGATCTAGATATAAAGAGAGCACCAAGATTTCTCCAGGTGAT
CTATTGTGTHAACCATACAGATATACTGTGAACGTTTCCGCCAAAAGTTTTCGA
TAATGTTATATAAGGTAAATTCAGCTCTGTCGAGCAGCAGCCCAATAAATTT
THACAAATCATCAGTTTATATCTGTAACACAGCATATGGAGACACATATT
GAGGTTTCGCGAGATTTATGTCGCGTTTCAAAAATATCTGTGTAGTGCAGCAA
AAACATGATTTCTCCTACCGGTATATCTGTCGATAGAGAAATTTGCTACCTTTA
ACTCTTCAAGCGCAACGGCTTTTAGGCCCCCAAAAGTATCCCAAGTTTGATTTGT
TGTTTTGTGTGGTAGTAAATATCTCTAGCCCAATCAATCATCTCTTAA
CAATGAATTTGACGCTAATTTGTCTCAAGGCTTTTCATCCGATTCCAATATTA
CATTHAGAAGTTTATAGTACAGAGCCAACTTATCATTTTATTTACCGGTGAT
TTCTTGTCTCTGTTTTCAGACAGACAAGGTTTGTGAATTTAGACGCTGG
TAGATATCATCTGTTATCATACAGACAATGGAAGAAAGTTGTGTATCTCT
TGATAAATACGGTGAAACTTACCGGTCCAAGATCTCTACAGTTTCTTCTGTA

YBR019C. 699 aa (SEQ ID NO 40)

MTAQLOSEBTSKIVLTGGAGVIGHSTVVELLENGVDCVWADNLNSVTD
SVARLEVTXKHPIPFVVDLDRKGLKYEKZVSHVIFRAGLKAKS
TOIPLRYTHNNILGTJVLLELMQVNVSKFVPSSSATVYGDATREFNNIP
IPEECPLGPTNPYGHTKYAIENTIDLNSDKRSKWKFALLRFPNIGAHF
SGLIGEDPLGINNLLPYMAQVAVGREKLYIFGDDYDSRDTGTPRDYVH
VVDLAKGHATAALQYLBYANNENBGLCRENNLGSQSGSTVEVYHAFCKAS
IDLKPVYTRAGQDVNLNTAKPDRKRELLKMGTEQLQZEDSKDCKWMTTE
NPFYQOLRGVEARPSAEDMRBYDARVFTVIGAGTRFQATYANLGASVLDLV
NQSVLVGENEEGYLPNDPSAVIGIATGRYANRISKGFSLNCKDQJLYT
NNGVANNHSSIGSEPHRKFRLIYNQPSKQVPTAEMLIDNEKDTDFPGD
LVLTJQYTVNAQKSLEWYKGLTAGENATPLNLTNHSYFNENLKPJGDTI
EGTEIMVRSKSSVDNDKMIPTGNTVDRLEATFNSKTVLPQKPNQFQDC
FVSDENAKPSQIINNELTLVIAKAPHDSNTLEVLSTFTYQVYFGD
CLVADENAKPSQIPFRYDAIDAINENKDKCVTLKNGETYSKIVYRF
FLSVDENAKPSQIPFRYDAIDAINENKDKCVTLKNGETYSKIVYRF

YDR345C. 2204 bp. CDS: 501-2204 (SEQ ID NO 123)

TCTATAGCTATATATCTTCTTCAGAGCTTCGGCTGCTGCCGGGTCACTGCTTCCTCGTG
 CAGGTAGTTTCTTCGGATTTCTGTCGCGCTCAATATATACCGAATAATAAAGAC
 CGGAATATCTTCTTCGGCGGATTCGGTTTAAACTCTCTGGTTCGGGATATATCA
 CAGAGAAAGCTCTGTCGAGAAATTTTTCAGATTTTCTCGCTTCTCCCGATG
 TTGGTATTTCTCGGAGGTCAATATATGACGCCCATTAATAAGCACTGTACACA
 ACGACTTCTTGAGAGAAAGAACACATCAATAACGATGTGGGACATTTGGGG
 CGCCATCAAAAATCTTGGGACTATATCCCAAGAGAAATTTCTTCAGAAAG
 AGAAGAAAGTCAAAGTTTTTTTTTTCGCTGTGGGGTTGCAATATAAATACAG
 CGCGTTTATTTCTCAGCAGAAATATCCATATCTTTACTTTACTTATAGCTTT
 TTCTAATAATAATAGATAACAAAAATTTATACATCTTTTATTTAAACAATCT
 ATGAATTTCAACTCTCAGATTTAATAATCTCCCAAAAAGTCAAGTGAGAAATCT
 GAACTGCACCTGCTTCGAAATAGCTCTCAGGTATATGAACATCGCTCAGAGAG
 AAAAAGGTCTCAGATGATTTTTCAGCTGAGGGCCAGCCACAGTATTACCT
 AACCCAAATCAGGTAAAGTTTCCATTTGATCTGTTGCTATCTTTGTTGTTGTTG

101/251

TAATGTTGCGCTTGGTGGTTTGGTTTTCGGTTGGGATACACTGGTACCACTT
CTGGTTTCGGTCCGCCAAACTGATTTCTTTGAGAAGATCTGGTATTAAGAAGCAT
AAAGATGGTAGTTATTTATTTCTTCAAGTTAGAACTGGTTTAAATTTGTCATC
CAATTTTCAACATTTGTTGCGCATCTGGTGTATTTATTTTTCGGTCAAATTTGG
GTGATATGTACGGTCGTAAATATGGGTTTGAATGTCGTGTGTTGTTATTTCTAC
ATCATTCGGTATTAATTTATTTCAAATTCGATCAACAAATGGTACCAATATTA
TTTCATTCGGTAGAATTTATTTTCGGTTTCGGTGTAGTGGTGTATTTGCGGTATT
TATCTCCTGTTGTGATTTCTTGAAGTCGCTCTGAAGAAATAGAGAGGTACTCT
TTAGTCTCTGTTACCAACTGATGATTAATCTTTGGGTATATTTTCTTTGGGTATA
CTGTACCAACTTTGGTACTTAAGAACACTCTCCAACCTATTTCTCTTTGGGTATA
TTCTCATTTAGGTTTGTGTTTTCGCTGGCTTTGTTTATAGATCGGTGGTAGT
ACTTTTCTCCAGAAATCCCAAGTTATTTGTTTGGTGTGAAGCTGTGTAATTTGA
CGAACGAGAGCACTCTTTTCCAAAGTTATAAGGTTTCCGCCACAGAGCAATC
CAATCATTTCAACAGAGTTGGGAAGTTATTTAGAGTAGTGTGTTGAAGAGCGC
AAGGCTGCTGGTTTCAGCATCATGGGTCGAGTTGTTGTCACCTGTGAAGAACT
CATGTTTAAAGCGTACTGATGATGGGTATCATGATCAACTCTCTACAAACAAT
TGACGTGGTAGATACTATTTCTTCTTACTATGTTACTACCGGTATTTTAAAGCTT
TGGTGATAGTAGATTTCTTTGGAACACTTATTTGTTTTCGGTGTGTCGCAAA
CTTCTCTCTACTATGTTGTTCTTCTGTACACTGAGTGTGTTTGTGGACGTCT
GTAACTGTTTGTATATTTGGTGCCATTGTTATTTGGTCTGCTGTATATGTAGTATT
TAGCTTCTGTTTGGTGTACACAGACTATAGGCCAAATGGTGAAGGTAAATGG
TTTCTCAAAGGTCGTGTATCTGTATGATTTGCTTTATGCTGTGTTTCTATATA
TTTTCTGTTTTCGTACCACTTGGGCTCAAATTTGCTTATAGTTTCTTTATTTCT
GAACATTTCCCAATGAGAGTCAAGTCTAAGGCTATGTCTATTTGCTACAGC
TGCTAAATTTGTTTGGGGTTTCTTGATTTGGTTTCTTCTACTCCTATTTATTA
TTTGGTCTATTTAACTTCTTACTACGGTTACGTTTCTCACTGGGCTGTATGGTT
CTTGCGCTACTTCTAGTTTCTTCTTTGTCGACAGAACTACAGGTTTGTAC
TTTGGAGAAGATCAATGATATGTACGCTGAAGGTGTTTCTTACATCGGAAGT
CTGCTTTCATGTTGGTTCCAACATCTCAAAGAGGTGCTTAACACTGAGTCTGAT
GCATTTGATGCAATGATGACCGCCATCTTACAAAGAAATAATGTTTCGGCGCAGAA
ATAA

YDR345C, 567 aa (SEO ID NO 124)

MNSTPDLISPOKSSSENADUPLPSNSQVMMNPEKGVQDDTQAEADQVLT
 NPNTKGAYATVLSICCVMAVFGFVFGMDTGTISGFVAQTDPLRRFGMKH
 KDGSTGLSKVRTGLVUSTFNTGCAIGGIIKAGLGDGCRKMGUJIWVVYI
 IIGIIQIQTASINKWQYFPIGRIISGLGQVTAIVSLPMLISEVAPKEMRGT
 LVSCVQLMITIGIFLGYCTNFTKTVSNVQWRVPLGLCFALWFLPMIGGM
 TFWPESPRYLVEAAGQIDBARSLSKVNKAVDHPDFIQOEIVLEIASVBEA
 RAAGSASGNGELFTGKPAFKRTHMGIMTOSLQUTGDNYFFPYGTTVFNA
 VGMDSDFSTSLVFGVNFVFTCCSLYTFDREGRNCLLYIGAIGWCCVYV
 YASVGVTRLNGBEGBGSSKGAGNCMIVPACFYFCFPAITWAPIAYVVIS
 EFTPLRVKSKAMSTATAANWLWNGFLIGFTFTPTGAINIFYXYGVFMGMV
 PAYFVVPFVPEYETKGLTILEVNDMTYAEGLPWKSASWVPTSGRGANYDAD
 ALMHDDQFPFYKMKFGKK

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAAACCAGAGCTTCCTTCATCCGGGGGGGCTGTGTGTTCTACATAT
TCACCTGAAGAGCTCCGGGATATTTTAAAGTTATACAAGGGAAGAATCGCGGCTA
GACTAGCAAGTCTTTAGGCTGCTTTAACTATTTGGATGGAGCGGATAAAGGCG
CCAAACAGATTGTAAAGCTTTAGACGCTTTTAGAGGATAGGATGATACGTTT
TCTGTATTAAGATTAAGCTTTGGCTGGGATAGCAACTTTGGCGCAGAGTATA
GAAGACCAAAAAAAGGTATATAAGGCGCAGAGAAGCTCTTTGTGAATGTG
TGTAACTTCTCTTCATGTGAATACAGTATTTCTACTTATCTCTTTAAATATA
TACAGAATTAAGACAGATAAACCAACAGCGTTTCCAGATCATATATATA
TCTTTTCTAGCTTAACTATATATTTTGTTTTGTACTCAAAAATAAAA

102/251

AAAAAAAAAACAACCTGACCGCACTAATTATTCATTAATTAATAAATAAC
 ANGTCCTCTTAATAATGATGCTACAGTAGATCTACTTCGAAGTCA
 AAAAAAATTCAGACAAGATTGGCTTTAGTACGAGATCCACCACTTA
 GACGCAATGCTCAGTCCGCTTTTGTATGAGATGCTTAAAGAAAAAT
 AAACGTCTATTTTCATCAAGCGGTGATGATCGCTTATTCGGGTGTA
 AACCGGAAGATCTCAAAGGACAAAGTATTTGTTGAAGAACCTTACTGA
 AAGACGAATTTGGTGGGTCCGGCAATTAACCAATGTTCTGAAGAAC
 CATTTATATTGTCATGATGATTTGCGAGATGGATCCAAATACAGATTA
 AAGTCCGGCTTTGTTGTCAGAGGCTTACACGCTTATTCATGACAAAT
 ATGCTTATTAAGACTTACAGAAAGAAATTAAGCCATTTGAGAGACTGA
 TTTTACTGCTGGAACCTGGTCAAGTTCACGCAATTTACACACCCAGG
 ATATGCTTCAAAAGTACTATAGAAATTAATCTCAAGCAAGCAATGGAATG
 ATCATTTAGTACCGAATACGCGGTGAATGAAAAAGGTATTTTTCAC
 AGTTATGTTTTTACTGATGCTCGTGACCATTAAGTTTAACTTTTATGCT
 CTTCGCGCAACGAGGTATTTCAAAACGCTGACCTTAATTTATCTTGGC
 CTAAAGTGTACCGGAAAAACACTTAATCCGACACCAATAGATTTGT
 GATCGCGATGATGAAACATTTGTGTCGACACATGCTTTCTTAATATCG
 AAGTGGTGTGTTACGCGCAAGTTAATTAATTTATCTCGCGAAAAAGGCTT
 GAAATTTTTCAGCTATCAAGTTTGTGTTCTGTTATAGAAAACTTTACTA
 TGACGAGAAGTCGCAATGATGATGACATGACATTCGCAAGTCCAGATTC
 ATACTAGATGCTCCATCCCAATGATGATGATTCGCAAGTCCAGATTC
 TTTTGGCGGAGCTCTCATCCAAAGATTTAATTAATGATCTCCGAACACTGAT
 ACCATTCATCTCTGGTTACTCTTAATAATGCTGGTACTGACGAAAGT
 GTCTGTAACCTGAAACCAATTTTCAATCTGTTTGGTACCAAGATCTC
 AGCTTGGACCTATGATAGTACGCAACATGATTAAGTACAAAGATCTC
 AACATTAAGCTATAGCTACTTATTAACAACCGGCTGGAATGCTCTCC
 TAGCATGCTGGGTAAACGTTGCCATGATGATGATGATGATGATGATGAT
 GGATTTCTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT
 CGATTTCTATCTTCAAGTACCTTACCAAGTTAAACGCTTTCACGCTGAG
 CTTTGTAAATCTCTGCTTAAACGCTGCTCAAGTGAATCCAAATGACAGG
 TGCATGATCAACTTGGCAACTGTTGTTGTTCAAAATTTCAAGATTTATC
 AAGACAGGCCACACAGATGATTAAGCGCTGCTCCTCAATTCGAGATTA

YKR097W, 549 aa (SEQ ID NO 264)

MSPTMNAIVGSTRSEVQKIRQELALSDVTTIRMAPAVLYENGLKEN
 KTVISSGALLIAYSVKTRSPKDKRLVEBPTSKDEIWMGPVNRKCSERT
 WMINERADYLTTRDHIYIVDAFAGMDPKYRIKRVICARAYHALFMTN
 MLIRTEELAHFGEPDFVWNAQFPANLHTODMSKSTIEINKFAMEM
 IILGTEYAGEMKGIPTVMFYLMFVHNHVLTLHSSANGIQNGDVTLPFG
 LSGTERTISADPHRLILGDDEHMSDHFVNIIEGGCYAKCINLBAEKP
 EIFDAIKFQSVLENVLYDEKSHVVDYDSSITTEMTCAVPIDYIISAKIP
 CLADSHPKNIIILTCDSAGVLPVSKLPEQVMYHIFISGYSKMGTEG
 VTEPEFTSSCFQPLALHPIRYATMLATKMSQKANAIVLNTMGVSS
 VYSGKRCPLKYTRAILSDIHDSLANEYETLPIFNLOVPTKMGVPAE
 LNPFAKNWSQGESKRYRGAVTNLANLFDVNFKLYQDRATPDVLAAGQFE

YMR173W, 1793 bp, CDS: 501-1793 (SEQ ID NO 313)

AAACAAGTGAACATTAATACATCTGTAAATCTACAAAAATCGTAGTG
 CTGTATTTCTTTTGAAGATTGAAAAAGTACGATCATACATCTCTAATTC
 TGAGAAGGGGTCATATGACGTAAATCAATCGTAAACAGCGTTTCGGT
 GTGCGCTGGCCCAACACAGTTTGGCGTGTGATTTTAAAAACCTTGC
 GGAAGGTAAGAAAAACCACTCCAGAGTTTCGAGATGACAAATCGCCCTT
 AACCTGTGGCCATYACAGCTTGGACCGACGAGAAAAAGGAAAAAG
 AATGCTGTACAAAGAACTCTTACACCACGTTGATTTCAATTAACAACG

103/251

CCCCCTTTCATTAATTAAGAAAGCATTAATTTTATGTAATAAAAAA
 GAATTTCTCGAAATATGCTTACATTAATTTTCTTTTGTAGACTAGGG
 CTTTAATAGACTGATTAATACGATTAATTAAGTAAGCAAAAAACAGCA
 ATGGTTTATTTGATTAAGTAGAACCAATTTGCTTAACACATAATTAACA
 CATGATTTCTGGCAATTAACAATCAAGCGATTTATGTTTACCAATGAGA
 ATPANGTCGGCGAAGATAGAGTCAATATTCATAAAGCAAAATCGGAGAG
 GACAGATTTGATTAAGATGAGTCCAAAGTTGTGCAACAATTTTCTTAATC
 CTCTAATTAATGACACGATCTCAACACATGATTTATGCTCTTAACAAC
 ACAACGATTTATATGTTCTTAACAACATGATTTATGCTCTTAACAAC
 ATGATTTCATATGCTCTCAACACATGATTTATGCTCTTAACAAC
 TGATTTCTAGGTTCTTCCAAAGAAAGAGAGCTTAAGCTTTACACGA
 ATGACGATTTGCTAGGCTTCCAGCAACAATGACTTTTACGTTCCAAAC
 AACATATCTTACGTTTCCAAACAACATGACTCTTACGTTCCAAACA
 TGACACTCTTACGTTTCCAAACAAGAAATTAAGCTTTTACGTTTCCAA
 ACAATGACGATTTCTTAATGCTCTTAACAATGATTTATGCTCTTCC
 AACAAAGAAAGAGTTCTTAATGTTTCCAGCAACAAGATTTGATGTTTC
 TAACAAGATGATTTATATGTTTCTTAACAACAATGATTTATGCTCTTA
 ACAAGATGATTTCTTACGTTTCTTCCAAAGAAAGAGAGCTTTATGTT
 TCTTAACAATGACGATTTGATGCTTCCAGCAACAATGACTTTTACG
 TTCCAAACAATGACGATTTTACGTTTCTTCCAAAGAAATTAAGCTTT
 ACGTTCTTCTTACGAGATGATTTATGCTTCCAAAGAAATTAAGCTTT
 TCTTAAGGTTCTTCCAAAGAAAGAGTTCTTATGTTTCCAAACAATGA
 CGATTTCTTAATGCTCTTAACAATGATTTATGCTTCCAAACAATGA
 AGAAGATTTCTTAATGTTTCCAGCAACAAGATTTCTTAATGCTTTCAA
 GATGATTTCTTACGTTTCTTCAACAAGAAAGAGTTCTTATGTTTCCAA
 CAACGATGATTTATGCTTCCAGCAACAACAATGACTTTTACGTTTCCA
 ACATGACGACTCTTACGTTTCTTCAATTAAGAAACAAGATTTCTTACG
 TCTTCCAACTTACGTTTCTTCAACAATGATGATTTCTTAATGCTTTAA
 TAGAGCGCTCTTATCAATACGTTGTCAGCAGATTTACTAA

YMR173W, 430 aa (SEQ ID NO 314)

MGLEPDKVQFPANSNMNMDSGNNNGDVTYKAEIMIGEDRNVQFSKIGE
 DRFDMESEKVRQFNTSINDNSNNNDYSGSNNDYSGSNNDYSGSNNDY
 NDYSGSNNDYSGSNNDYSGSNKKSSYSGSNNDYSGSNNDYSGSNNDY
 NNDYSGSNNDYSGSNNDYSGSNKKSSYSGSNNDYSGSNNDYSGSNNDY
 NKKSSYSGSNNDYSGSNNDYSGSNNDYSGSNKKSSYSGSNNDYSGSNNDY
 SNNDYSGSNNDYSGSNNDYSGSNKKSSYSGSNNDYSGSNNDYSGSNNDY
 SYGSSNNKKSSYSGSNNDYSGSNNDYSGSNKKSSYSGSNNDYSGSNNDY
 DDSYSGSNKKSSYSGSNNDYSGSNNDYSGSNNDYSGSNNDYSGSNNDY
 SNNYSGSNNDYSGSNNDYSGSNNDYSGSNNDYSGSNNDYSGSNNDYSGSNNDY

YIL057C, 995 bp, CDS: 501-995 (SEQ ID NO 217)

CCCAACAGATTTCAAGTCTGTGCTTAAACCATCGGCGCAATGAGCCCTAA
 AACAAATGAGTTATTAAGCAAGTATTAAGTATTAATTTCTGATATAAAC
 TACAATGACCCACGACTGCGGTGTAATGATGCAATGAATCAATGTAAC
 GAAATTTGCGGCTATAGGCTGAGAGGAGGACTTAAGGAGGAGGAAATG
 ATTAAATGCGGGTAAATTTGAATATGATTTAAACGGGACGCGGTTTG
 CATCAAAATGCTATTTGTTGGGTATTTCTCTTAATTTTGTGTTGGCTTG
 AACCTTTTGGCGGCTTGGCAATGCTCCGTAATTAAGCATCGGCTGCCA
 ATCTCTATTTGCTTTTCCCTTGACCTCTCTCTCAATTTCTGATATCT
 TTGCGCTTAAAGTATGATTTGATTTCACTTATCTGTAATTTTAAATTAAGA
 TCCAAAGAAACAACGTCAGTATTAATTAACAAGTATTTTAAATTAAGA
 ATGACGAAAAAAGATTAAGAAAGCAAGGCTCTAAGATGATTCACATTC
 TACAAAAAGTGTGATCTTAAAGGTTTGAAGATTTGATGATGATTTG
 AAACATATTTAAAGGTGAACGAGATCAAGATCAAGATGATTCATTCAT
 TGCCAATGTAAGTACTATTCACACCTTTGCTCTGATGATGCGCATGATTA

104/251

TCCGGAAAGATCAAGACACTGCCAATCGCACCTCTAAGAAGATTGTGTTCC
GCCATTACACCCAGCATGTTGAGAGACTGCTCTAAGAGACATCAAAACC
GCTATCAACAAGCAGAAATTCGAATTCACGATAGAAAAAGCAGGAATC
CTTTGACCGGATTGTTTGGAAATTTATGGCGAAGAAACGGAGTTGAACGCCA
AGAAAATCAAGGTGCTGCTGCAAGTTGTATGTAAACACGATGGCGCAATG
GTAGATGTTGATTACAAGACAGAACCCTTGCAGCCCACTCATCTAA

YL057C, 164 aa (SEQ ID NO 218)

MTKKDKAKGPKRSTIITTKSGESLKFEDLDHDFETYLYLKGTEDEQEDHVV
CQLKYYPFVLHDHDDPEKIKETANSISKKFVRHLHQHVEKHLKLDIKT
AINKPELKFHDKKDFDRIVWNVGEBTELNAKKFKVSEVVEVCVKHDGAM
VDVDYKTEPLQPLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTAGCTACTTTCGTTTCAATTTCCATGGTGACACAGTAT
CTTAATATCTGCTAGTCGAGGAGAACAGGATTCCTGTGCTGCTCAG
CCGCTTCGTGGATATTCCTCTGGATATCTTAAATATGAGCACTACGCTTAG
CTCGCCTTAGCCCTACAATTCCTTCGCTCTCGAAGAACCAATATAATA
GAAAGTTATAAATTACATTTCTTATTAGTATACGACCTCGCGCTTCGA
AGTAGAGAGCCCTTTTGGGCTACTACATATGCGGCGTCAGACAGACA
AACTTCCGCCAAAATAGATTTACCCCGCGGAATAAGAAAACAGACCAATT
CACCACAGGATCAAGTACTTCTTGGTGCAATGTCCCACTATAAAA
AAATTCCTGACCTAGATCTGGAGCTAATAATCTGCGTCACAATCGCCT
AAACAGGAATATTCCTATTTTCGTACAGGTTACTTCTAGATGCTAT
ATGTCCCTACGGCTTCTCTAACACCACTCAGCATGCAATACAGTGACAT
ATATATAC
CCAC
CCAGAGAAGCCTAAGCCTAAGACTAAGACAAGCAAGCCTGACCAACC
TGCTCTCAAAATTACCTCCATTAACCTTACCTCCCACTGTTTACCTGTA
CTCATTAACATTAACACCAACCAACCACTCACTCCCTGCTGATACAC
ACCAACGACCGTCCACCACTACCGTTACCTCCCAATACCACTATCCAA
CTCCACTACCACTACCTACCACTCTCCCACTACTACTACCACTACTAT
TGTTCTACCCACCACATATTGAACGCTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTPSSMQSDIYIHTPHPHPHHHTHTPTPHPHHTPT
PERSLSLRQAKPDQPSVQIHLHYPTSLVTLTHSTIPPPPSISLCTT
TNRPSITVTLQLPISNSTTYPISHLULLLILLYPYPPLKK

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

GGCTTTTTCAGTCCGCGCGCTCGAGATCCAGGCACACAGGAATAGGCA
CGCTGTGATTCTAACATAGAGGGCTAGGCCGCTGACGTGGGCTC
TAGTTCCACTTTTCACTATCTTCTGCTCTTCTTCTGCTCCACAGG
CCGTTAATGGCCTGAACAGATTTTGTGACTTTGGACTTATGATAAGATG
TTTGTCGGGTGCGCGGATCTATCGCGGCAATCAAGTCTAGTCTGT
TTGCATCATCAAGGCACTGCTCATTTGTGTAATTAATTTCTAGCCTTTG
TCATCAATATATATAACTACAGCGCTAGGAGTGGTGTGCTGGCAG
TGGTAAGTAGCGGCTGCTTTTGGTCAATGCGGCAATACTGTGCAACGG
CCCGCGGTAGGTTCTTCTGGCTTCAACCTTAGAGCTGATACCTTTTGGC
TGGTCAAGGGGAAAGCTTACTCTCGCTTTCAGTCTGCTTTTCGCTTTC
ATGCTGCTATGCTTTACCGTACTCTGCTGCTGCTGCTGCTGCTGCTGCT
AGCTGCTATGCTTTACCGTACTCTGAAAGGAGTACGCTCATGATGTT
GTACCAAGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
CATGCCCACTGGTACAAGCGGTATGGTCTTTTCTTCTTCTTCTTCTTCT
GACGTGGGATGGTTCTGCGGACCAATCGCATGGGTGGTGGATGTTG
TCTTTGCTAGTTGCAAGGTAGTCTTCTTCTCTCTCTGCGCTTCTGACGAA

105/251

AAATGGCCTTACGTATCTTTTTCGGCGTCTGCTGCTCATCGCTGTTCA
TATATGCTGCTGCATCATATCGCGCTTTTACTGCTGCTGCTCTTTTGA
AGAGAGTTTCAATTGAAAAGTAGTGAAGAAAAAAGAAAAAAGAAAAAT
AAAAAGGAAAAAGCTTACATACGGAAGAGAAAAAAGAAAAAAGAAAAAT
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSQVASFALGNTLVACYAFTVLEKRSMTSCTNALSFLFFLLTLRRI
HRHWKPYGAPLLILFVLTLBWFRGPAAWVVVVVVFASCNVVFSPALSD
NWPYVSFFGVVVVIAVIIIVTHIGAFACCLLKRSLKSESEKKKKKK
KKEKSLHTEREKKKKKF

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCGGTAGCTACTTTCGTTTCAATTTCCATGGTGACACAGTAT
CTTAATATCTGCTTAGTCGAGGAGAACAGGATTCCTGTTGCTGCTCAG
CCGCTTCGTGGATATTCCTTGGATATCTTAAATATGAGCACTACGCTTAG
CTCGCCTTAGCCTACAATCTTCTGCTCTCGAAGAACCAATATAATA
GAAATTTAATAATTAATTTTCCTTATTAGTATACGACCTCGCGCTTCGA
AGTAGAGAGCCCTTTTGGCGTACCTACATATGCGCGCTCAGACAGACA
AACTTCCCCAAAATGTATTATACCCCGCAATAAGAAAAACAGACCCATT
CACCACACAGTATCAAGTTACTTCTTGGTGAATGTCCCACTATAAAA
AAATTCCTGAGCTAGCTAGTCTTGGACTTAAATCTGCGTCACATCGCCT
AAACAGGAATATTCCTTATTTCGTACAGGTTACTTCTAGATGCTAT
ATGTCCCTACCGCCTTGTCTAACCATCCAGCATGCAATACAGTGATAT
ATATATACCCACACCCACACACACACACACACACACACACACACAC
ACCCACACCCACACACACACACACACACACACACACACACACACAC
CTATTTCTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPCLTPSSMQSDIYIPTPTHTHTPTPHPHHTHTHTHNPNT
LP

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCAGTATCCCTTTCTGAATAAGCTTAAACCTTGCAACCCAGGGGTG
CCGCGCTCTTAACCTTTCAGCCTCGCAGCGCGCTGAGTCGCCGAATGTTG
CGGCGCTGCGCCCGCCGCAACACCGCGCCCGCTGCTCAGCTTAACC
GAAACACACAGGCTGCTCATCTTCCATATACCTGCTCTTCTTCTCACA
ATGCCGCTCAAGAGCAACTGCAAAAGAACCCCGCTTAGTGGGTTT
TCCCACTTTGATATAACCCCGCCCGCCCGCCCGCCGCTCAACTGGTAA
TTTAACCAAAACACCGGGTCAATAATTTAAAGCAAAACCTTAAAG
CGTTCTCGAAGAAATCTTCTGTAGTATGATGCTGAGCAAACTTATCTTT
TAGAGTGTGTTGCTTACTGCTATGCTAGATCAAAATTTACGTAGCGGCC
CTTTCAACCCCTGCGAAGTAGTACATAACAGCAGGTAGTGAACGCTG
ATGTTCAAAATACACGTACAATATTAATATACAAATAGTAAGGTGATGA
CAGACACACACACACACACACACACACACACACACATATATATATA
CAGAGATCAAGTTAGTGTGAGGAGCGACTACTGAGTTTGAAGTTCTTT
AAAGTGTAAAGTTATTTTCCCTCTCCCACTCTGCTGCGAACCTCTCA
CCACCCCTTAGCAGCATGTCTCCGTACATGACCACTACCTCAGCAATACT
TATACATAAGCAAGATAGTTCCAAAGCTGCTCTCAGTGGCGCTTACTCGA
CACCACACAGAGAACTTGTACTACGAAAAATAGAGAAATCGACGCGGCTTACTCGA
GCTGGACAGGATCTCGACGAAATAGACGAAATCGACGCGGCTAGTAC
TGTGTGACGCTGCGGAGTGTCTTCTACTGCAAGAGCTCATTTCCGCTTCC
CCAGCATCCAGCAGCTCTTCTCTCTCTCACTAATAACATCCGGCCCATAG
CATATGTGA

108/251

ATTGAAGCTGTAGTAATATACAAAGCCCTTTTCCAAACATTCGGTTATGCTGCGGACGCAATCTCAGAAA
CTCCGAAACAAATAGATTAATACATGATTTCTTATAACTTAATTTTGAATTTATTTCTTATATATAC
AGACAGGTGTACAGATCTCGTACTCGTATACATGTTCCAGGTGTAATCTCAGAAAGATGTCGCGTCCAT
CTTTCTACTTCTGAGCTTACAAAGTGTGGTACATGTTGCGACATCAAGCCAAATGGTCTCATCCAA
AAGGTATGCCACACAAAGTTTACCAAGGTGAAGACGGTGTCTTACAAGCTTACTTAAGTCTCTGTT
GGTGTATCATACACAGATGGTGAACAGTATCTAGAAAAGAGTAAACTTAAAGTGTGAACAC
ATCAAGCACTCCAAAGTGTAGACAAAGATTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGTGAA
GCTAAGGCTCAAGGTGTGCTGTTCTCAATTGAAGACAAACAGCTCAACCAAGAGATCCCGGTATGTT
TCTACTGAAGGTAAAGTCTCTCAAACTTTGGCCCGCAGTTCCTACAGAACTTTTCTATCTAA

YBRI91W, 160 aa (SEQ ID NO 62)
MGKSHGYSRSTRYMFQRDPKHAHVLSTYLKVKVKGDIVDIKANGSTQKGMHPKFYQGTGVVNVTK
SSVGVIINKVMGNRYLLEKRLNLRVEHIKHSKQCHEFLERVKANAAKRAEAKAQQAVQLKRPQAPRES
RIVSTEGNVPTLAPVPYETFI

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAAGAAACCCCATGTTCTGTTTGGCTGCTCCAATGCTTATATCACTCTCACTCTCACTGTCACAAT
CGTGTGCTTCTCATCTTAGAAAGGATACACATGTAATAACAATATTAAGATTTAACTTATACCT
TGATCACTTTACACGTCGAAGTCAAAACAGTTTCATAGTTATCACTTGAAGTAGGCTCCATCATCTA
TAAACATGAACCTTCATGCAAGTGAAGTGTCTACAGATAACAGACGCGCAAGCGGTTTCCAGAT
TGCGATGCTGTTTCTTATCTACTGCTTACTACCCCTTACTACCCCTTGGCCCTCTGATTCACGTGAT
GGGAATTTTGCTTGAAGAGGATATATATAATAATGAAGAAGTTTATATATAATAAAGGAGCT
TTAGCATATAATAAGAACTCGTGAGTACTTATACGAGCATTCGCATATATATACAATAGACAAAA
CCTCAGAAAGGAAAAAATGTTATCTCAAGAACTATCAAGCAGTCAAGGACCTTATTCGCAAAAACG
AGATCTGTCGCTCCAAAGCTGCTCCATCTGCTACATGCCATGAGCCCTAAAACAGCTTTTGGAAAAGT
TAAAGTTCACAGTCCAAAGTCTGGTTTGGCAATTTGAATGATCATTAAGGAAGGGCGACATTCGAG
CTGCTGTTATGAGATTAATGCAAGAACCGTGCACCAACATCTATATTAATGTTAAACATATTCGG
GCAACGAGCTTGCAGGAATTCGAGGAGACTGGTGAATTCGAGGAATTTGTAGAACCTATTCTTGCAA
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSEETIKHVXDLIAENELFVASKTVCPCYCHAALNTLFEKLKVPRSKVLVLQLNDMKEGADTQALYEI
NGQRTVNIYINGKHIGNDLQELRETEGEBLELLEPIAN

YDL004W, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATAAACATAAGATATATAGTTTTTAAATGGTCAAGTATGCCATGCAACAACCTAAAAGGTACCAATTC
ATTAAATATTATTAATTTACTTTCTTACTATTACAGAAAGACAAAGTGTGAAATGCCTAGGAGATTGAT
GATTCACAAGCTCTGGCTTGGCAATAAATACTTATACACAACCTTCAATATATAGAAAAGAAAGAA
GACTATAAGCTTAAATAATGAGCAACCTTCATTTAAATATTAATCTTAGGACTTGGTAATAATAGCTAAT
TTGTATATTATTCACCTCGTCAAGCTGTATCACTTTTACGAAATATAGATGCCAGCCCAATCAAA
GCCATTTATGAGTGTCTAGGAAGGGCGCTCCCATCATTTGTAAGTTCATGTTTAAATTTAGATGGAG
GATTAACAATAAGGATATGTCACACACTGTCAAAGAGCCCTCAATCAATTTGTGAAGTATATCTGTA
CGCTGAGGATAGGAAAATGTTACGTCAATATTTGGAAGAGTGCATCAAGATCAATGCAATTTCTGTCG
CTAAGCGTTCATATGCAAGAGTCTGCGCCATCATCAGGTTTGAAGTTACAAATTTGCTCTACCAACG
AAACTTTATATAGTGGCTCCGAAGTTACTCAAGTACCTGCCCTTGAAGTGTGGAAGTGTGGTGTAT
TGCCCAACCATTTCCCTCCAGGTTGAACAATATCTACCGAGTGTGGAAGTATAGGAAGGCTCTAATC
CTAAATAATCTTTATATCAGGTGGATTTGCAACAGTTCACACAGTCCGAGTATATGTGTACTGTCAA
TTGAAGCTTTTCCATTTGGAATCTTTTTCACAGAAATATATAAATAATTTGTTGGCAGGAAGCTTAAGAAG
ACGTGTATTCATCTGATGCCAGGGAAGCCGACGAAGTGCATATTCAGTAGAAGTTTTAGAAAACCTAC
AATCCGTATTGAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRSLNFVARSVAEAAAASGLKLQFALPHETLYSGSEVTQVNLPAKSGRIGVLANHVP
TVESQLLPGVVEVMEGNSKKFTISGGFATVQPSQLCVTAIEAPPLESFQENIKMLLAEAKNVSSSD
AREAAAAIQVEVLENLQSVLK

109/251

YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263
(SEQ ID NO 85)
ACTATATTTGTTTTTCCCGAACCTCTCCCTCTCTGGCCCTTTTTCATATATTCACAATATTTTTCATPAC
CTTTTACCTCCGTACACCAATCTTTATTTTACCCCATACCTTTGTATTTCTGAAATTTGAGAAATGATTT
GTGGTGTGTTTTTTTTTGGACATCTGCTCTGTGGACAGTTTTTGGAAACGCTAGCGCAGCATGTTTGGAA
CGGAAGGAAGTGGGAGAGCCCAAGAAAGCTTTCTCTCGCATGGTGTGATCTATTTCTGCGCAGCGGAGGAT
GGGAAGCTCCGTTTCAAGTCTGCGGCTTTTCTTCTGGCCTTTTCTTCTCCCAATTCGCGCAGCAGAC
ATAGCTTGACTTTACTCATGCTGCGCATTAGGGGTTTGAATCTCATAGCTTTGAAGATAGTATTTGAATTT
ATATTGAAGATTTTATATATAGTGAATTAATTTCAATTCAGTTTGAAGAAAGAAATTAATTAAGCAACAGA
ACTCAATCAAGGAATAAATGCGGTTTGAAGAGAGTGTCTACCTGTGAATACACCATTAATTAATTCGACA
AAAGATATGGAAGAATAAATAATATAATGCCCCAAGGCTGTCTCATCTGAATGTTTAAATAGAAAGAT
ATTTCTATAGTCAAGGAATACAAATATCAAGAAATTTGTACCACAGAACCTATCAACAAGATCATTTGAT
CAAGATATATTTATTAATACGAATTTTGAAGACCATTAATCAATATATATATATATCAAGAGGGGAAGAT
ACACTTCGGCTGGACTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGAATCTCTAGATTT
TAACTCGCAATATATCCATATCCCAAGTTTGACTAAATATGAAATCAGAACAAATTTGGGTCTCCCAATATA
CAAAACCATTCATCAAGATTACATATATATAAATCAACAATCGTTACTTAACAAAAAATTTTACCATT
TATTTTAAATAGTTGACGGTGTCTCTTCAAGAAGAGCTTCCAAGAGCTGTCAAGGAAATTTAAGAAG
TTCCCAAGTTACACATGGTACTGATGATGTCCTGCTAGCTCAGAAATTTGAACAACAGCTATCTGGAAG
AGAGTGTCAAGGGTGTTCAAATACAGATTAAGATTCAGAAATTTCCAGAAAGAGAAACGAAGAAGACAG
GCCAAGAACCATTTGTTCTCTCTACGTTGAACTGCTTCTAGTTGCTCTGCCAAGGGTCTACAAACTGTT
GTTGTCGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGLKDVVTREYTNLHKLHGVSFKKRAPRAVKEIKKFAKLHMGTTDDVRLAPELNLQAIWKRGVKGVEY
RLRLRISSKRNEEEDAKNPLFSYVEPVLVASAKGLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495
(SEQ ID NO 89)

TGACGGTCTTTCACAGGAATGGAAGATGCTTTTATGCGCGCGCATATAGAATATGATCAGAGAGGATGCG
GTACTTTTAAATTCATAGAGTTTCTTTCAGGTTTGGAGGTACTCAGACGTTTGAAGAAATTTGAGGAGC
AATTAGAAGTTGTAGTATGATCTATCTTAAACACTTAACTCTCTCTCTATATCATGTAGTGTACTTTT
AAACATTTTTTTTCTTCATAGCAATATATAGCCTTTTACCACCATTAACCATTAAGTAGAGACCCAA
ACATTTTTTAAAAAATTTAGCTTATATTTTCTTCTGCTTTTCTGCGCGCGCAAGATGAGCGGT
GAAATTTTGATACGAATGAGATTTCCACTCTCTGATAGATGGAATTTTATGTTGCGCGCATATATCAC
AGTGTGATGAATTTAAACATTTCTTCTCTCATTAATATTTTCTTAAACGGTTTAAACCATTAATCAATC
AACACAATCAGTCAAAATGGTGTGATGCAAGTGCCTGATGTTTATTAACACCATAGGAGATATTA
ATGCAAAAGTTGCAATGTAATGTTCTGCTTAAATCAGATGACACTTAATGTGGAATTTCAAAAAGTGGATTT
CTAATATAATTTGCTCTGTCGGATCACAATTTCTATTAAGAATTCGCTGCTGTCACAGGTATATGTTTA
TACTGGAGAGTATGTTTCTACTGCTGTACATTAAGTGGGTGATTCCTCAATTTCTTTTACAAATATGTTGC
ATTAGTTTAAACAGGTTATATCTGCGCTTCTCAGTATAATTTTACGCCGGAATAATTTACTGATGGCTA
GCCGCTTTATGAATTTAACTTTTCAAAAGCTCATTAACATACACAGCTTAAACCTATCGGAGGAACCAAG
ATTGAAGAAATCACCGGAATAGTTATCTTAAATGGAATTTGATATGCTGTGAACGAGGAATAATGTCATG
ATACACTTTTCTCAAGCCATATGTTATCTTCAATGATCACTTAACATTCGATATAATTTTGTGGAATATCCAA
TTCCACTTAATATTTTAAACAGGTTAAGGATTTCTTCTTCTGCTATTTCCATCTCTAGAAATGCT
TCCAGCTTGTGTTCAAGTTTCTCTGATCTGCAATTTGAACAAATTTGCAAGTACGCGGAGAAAGGTTT
GACTCCATCTCAATTTGTTGTTGTGAGAGTGTCTCAGGTTTACCAGCTGCTGTGTATCATCTG
TAAACAGATCAATAGAAATCTTGAAGTCCAAATGTTGCTGTCGAAATTTCCGAAATTTGTACTACTTT
GATTAAGAAGCTGCTCTCTGTTAGAAAGCACTTGGAAAGAAACAGAAAGGACAAAGACCGCTAAGTTTACG
ATTTGATTTTGAATTCAGATTTACAGATTTGGCGAGATCTACTACAGAACTGTTCTCTCTTACCCAC
AAACTGGAAGTACGAATCCGCCACTGCGCTCCGCTTGGTCACTAG

YDR064W, 151 aa (SEQ ID NO 90)

MGRMHSAKGKGSIAFPYSRNPAPWFKLSSESVEIQIVKYARKGLTSPSIQIGVLLRDAHGVTOARVITGN
KIMRLKSNGLAPEIPEDLYYLIIKAVSVRKHLERNKDKDAKPRLLILIESRIHLRARLYRTTAVVLPNN
WKYESATASALVN

112/251

ATAAATCAATAGTCAATAGCTCCCAAGTTTGATCCAAATGAAGTTAAGTAACTGTACTGTGAGAGCTG
TCGGTGTGAAGTGGTCTTCGCGCCCTTGCTCCAAAGATCGGTCCATTGGGTTTATCCCCAAAGA
AGGTGTGTAAGATATGCCAAGGCCACCAAGGAATTAAGAGTATCAAAAGTACTGTCCCAATGAAAA
TCCAAACAGACAAGCTGCTGCTGTTGTTGTTCCATCTGCTTCTCTTGTGCTTACTGCTTGAAGG
AACCCAAAGACAGAGAAGAGTAAGAACCTGAAGCATAGCGGTGAACATAAATTTGGATGAATTA
TTGAAATTCGCCAGCAATAGAGACAATCTCTCGGTGAACCTTTGCTGCTCCGTTACTAAGGAATTT
TGGGTACTGCTCAATCTGCTGGTGTGTTGATTTGAATTTCAAGAACCCCTCATGACATCAATTGAAGGTATTA
ACGCTGGTGAATTCGAATTCAGAAAACTAA

YDR418W, 165 aa (SEQ ID NO 132)

MPKFDNEVKYLYLRAVGGEGASALAPKIGLPLSPKPKVGDIAIAKVFKEIGIKVTVLKIQNROA
AASVPSASSIVITALKKEPRDRKDKNVKHSNIQLDEIETARQMRDRKSFGRTLASTVTEILGTAQS
VGRVDFKNPHDIIIEGINAGEIEIPEN

YDR513W, 932 bp, CDS: 501-932 (SEQ ID NO 133)

TCCTCCCTCTCGCATATAACCCCACTGGTATTTTCCAATGCTTATTTTGGAAACCTGATCTTAT
ACCAATCTGCACATTTACAGAGGTCAATGCGGTGGATATACAAAACTTGAATTTGGACACCTGCTTGT
CAGATGATGAATCTCCATATCTGTAATAGCTTCTAAATTTGCCCTCCATCGAATGAACACTCGTCA
GTGATCAAAATGCCCTCGGCACTCATCGTTGTCGGATATTTGTACTCATCTCTCTCTGTTCTCTCC
TCAAGCTGCTCTTTTACCTTAATAGAACCATCGCTCCCTCTTGATTTATGTAATACACATCCAA
TAGCAGAACTATTAATAAGATCCGATATTCGGCCCTCTCGCAAGGGCCCGCCGCTTCTCAT
GAATTTTCATATAAAAGTCCAGAGCCAGAAAAGGTGCCCTCTTGATTAAGGACACTCCAACTA
CTGTTATATATTTTTCATGAGACAAATTTTCTCTGACTCGAATTTAATTTGTTATATCATCA
CGTTGTTGCCACAAGATATTTGCTAAAGATTTTTTATCTCACAATAATGGTATCCAGGAAGACG
TTGCTCAGTAAAGATCTGATTTGCCAAAGGAAGTTTGTGACAGCAAGACATATGCTCTTACT
GTAAAGCTACTTGTCTACCTCTCCAGAATTTGAAGCTTCCAAATCCAGGCCCTTGTGTTGGAAT
TAGATGAATTAGCAATCTGAGCAATTCAGACGCTTGAAGAAATCTCGGCCCAAAAAAGTTAC
CTAACGTATACATCAATGGCAAGCATTTGGTGAACCGGATTTGGAACCTTTGAAGAAAAATGGCA
AGTTAGCTGAATATGAAGCGGATTTCAATAG

YDR513W, 143 aa (SEQ ID NO 134)

METNFSFDSNLIVIIITLFPATRIIAKRLSPKMKVQSQETVAHVKDLIGQKEVFAAKTYCPYKATLS
TLFQELNVPKSKALVLELDENSGSEIQALBEISQKTPVNVYINGKHIGNSDLETLLKNGKLAEL
KPVFQ

YEL009C, 1346 bp, CDS: 501-1346 (SEQ ID NO 139)

AGTTTCACTAGCGAATATACAACTCACCGCCACAGCTCATCTACTTCCGCAATCAAAACAAA
ATAATTTTATTAGTTCAGTTTATTAAGTTATATCAGTATCGTATTAATAAAATTAAGATCATTTGAAA
AATGGCTTGTCAAACCGATATATTTTGTGTTTAAAGTAGATTAATTAAGAAAATTAATAAGAAAT
ATGTGTTAAATTTATGAAGAGAAATTTATTTTCCCTTATTAATTAAGTCCCTTACTTTTGTGAA
AACTGTCAGTTTGTGAAGAGTATTTGTTTGTATACCAATGCTATCATGTCCCGTAGAAATTTTAT
CAAGATGTTTCCGTAACGGTTACTTCTGTCAAAATTAACAGGTTTACTCGCCCAATAAAATTTCCCT
ATACATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AATTAATACAAATAAATGTCGGAATATCAGCAAGTTTATTTGCTTTAAATCCAAATGGGTTTCTAC
CATTTGATGTTTAAATTAATCAACAGAAATGTATCTGCTTCCCTTACTTACGCCAAACCAATGGTGG
GCCAATGTTATTAATTAATCAACAGACTGAAGAGTCCAAATTAATCAACAGAGTACCCCTTCA
ACCTTGATTTTGTATTTGCTCTTCAACAGCGCAACTGCACCTGAATGCAATGCTTTTGGCAATTC
CGGAGCTAGATGACGCTGTAGTGGATCTTCTTTCTGTCAGCACTGATTCAACTCCAAATTTTGAAT
ATGAACCTAGAACCAACTCTAAAGATGACATCTTGTGTTGACAAATGACATTCAGTTTACCATG
ACGATCTTTTACTTGGCTGATAGGCAATTAATCCACTGAGAGATTTCTTGTGATACCATCAATCTGG
AAGTCTGCAACACTTACTTTTACCTCTCTGTTCTAGAGATGTTAAACTGACTCAACAGCAAGAAAG
TTAAGAAACCAAAATCAGTCTGTAGAAGTCACATCATTTGTTGAAGAGATGACCAATCGAGACTGGATC
ATCTAGTGTGTTGTTTACAAACCGCAACAGCGTTTCGATTCACATTTCTCCAAATTTGCGCCGAATCCA
GTGATCTGCTGCTCTAAACGTTGCTAGTGAACACTGAAGCGCGCGGCTTCTGTCGGAGAAAGTTGC
AAAGAAATGAACACTTTGAAGCAAGAGTTTGAAGAAATTTGCTTTGCAAAAAATTTATCATCTTTGGAATGAGG
TTGCCAGATTAAGAAATTAGTTTGGCGAACGCTGA

113/251

YEL009C, 281 aa (SEQ ID NO 140)

MSEYQPSLPALPMGSPLDGSKSTNENVSASTSTAKPMVQLIPDKFLKTEEDPIIKQDTPSPSLDPDF
ALPQTATADAKTLPILPELDDAVSFSSSTSTPMFYEYENLEDNSKEMWTSFPNDIPVTTDDVSIA
DKAIESTEVSIVPSNLEVTSTFLPTPVLADAKLTOTRVKVKPNVSVVKSHHVXGDDRESRLDHLGVVA
YNRKDRISPLSPITVPESDPAALKRANRTEARRSRARKLQMRKQLEDKVEELLSKNYHLENEVARLKK
LVGER

YGL123W, 1264 bp, CDS: 501-1265 (SEQ ID NO 163)

TGGCTATTCTCACTAAGGATCTTAAGGTTTCTTAATAGTTTCTACGTCGGCATCGGATTTGTTGGTT
TAGAAGACTGCTTTCTAAATATATGTTGGGTGTTAATTAAGCTAGACCCATACACCCGCTCTATGGGATTA
TTTACTGTTTGAATTTAAGATTTGATGAATTAAGAACTGGACGCAAACTATTGATGGAACCAAGCATGT
CATCATTAAGAGGTAACTGATCTGCTCCCTTAGTATTGTCACGCAAGTTCCTCCAGGACCGCTAG
CTATTTTTCTCATCTATCTCCCTCTGTATTAAGAGTTTTCAGAGTTTAAATTCAGACTTTCTCTT
CTTTGTTTCCAATTTCTCTCTGCTGATGATCACTTTTCAATCCCAAGAAACCGTGTCTTTATTA
TATCTGCAATGAAGGTACTATCACTTCCGTTTCCATTTCCGACTATTAACAACAACCACTATAA
GCTCAATTAATTAAGTAATGCTGCTCCAGAGCTCAACACAAGAGAGAGGTGTTTGGTGGCCGTA
ACAGAGCGCTCCAAACAGAGAGGACCAAGAACTGAAGAAAAAGGATGGTTCCAGTTACCAAAAC
TAGGATGATTAGTAAGGTGTAAGATTACCACTGAAGAAATCTTCTTGCACCTCTTGTGCCAGTCA
AGGAATTCAAATCATTTGACACTTTTGTGTCAGGTTTGAAGACGAAGTCAAGAACATCAAGCCAGTTTC
AAAAGCAACAGAGCGGCTCAAGAACCAAGATTAAAGCTGTTGCTGTTTGGTGACTCTAACGGTC
ACGTTGTTTGGTATCAAGACCGCAAGGAATTTGCTGTCCTCATCAGAGCTGGTATCATTAATTTGCCA
AGTTGCTGCTTATCCAAACAGAGAGGTTATCGGGTACCACTTGGGTCAACCACTTTTGGGCCA
CCAGACCACTGATGATGTTGTTGCTGCTACTGTTAGATTGATCCAGCCCAAGAGGTTCTGTGATCG
TCGCTTCTCAGCTGCAAAAGTTGTTGCAATTTGGTGGTGGTGAAGATGCTACACCCAACTTAACG
GTAGACTAGAACTTTGGAACCACTTGAAGGCTGTTTCTGCTGCTATTTGTAACACATACGTTTCT
TGACTCAAAACTTTGCGCGCGCAACCACTTGCCAGTTTCTCCATTTGGACATCTACTCCGATGAAGCTT
CTGCTCAAAAGAGAGATTTCTAA

YGL123W, 254 aa (SEQ ID NO 164)

MSAPEAQQRKGGFGRNRRGRPNRRPTEEXGWVPTVTKLRLVAKGKITTIEEFLHSLPVKEFQII
DTLLPGLQDEVNMIKPVQKTRAGQTRFRKAVVVVDSNGHVGLGIKTAKEVAGAPRAGIIIAKLSVIP
IRRGVGTNLGQPHSLATKTTGKGSVTVRULIPAPRSGSIVASPAVKLLQLAGVEDVYVTSNGKTRTL
ENTLKAFAVAIGNTYGTLTNLWAEQPLVPSPLDIYSDASAQKRRF

YGR209C, 815 bp, CDS: 501-815 (SEQ ID NO 187)

AACATCCAGACTTTTAGGGTGGCAACGGAACCAAGCTATTTAGAGATTGTTTTTGGTCAAGCGAGGA
ACCCCTGTTGGCAAGTTGCAGATATATCATGGTGGCGAGGTCAACCATTCGAAGCAITGAAAACCGTT
GGCGGCTGAGACTAGTGAAGAAAGTCTTGTGAGCCCGGTAAGAAATGACATCTCGGCTTCAAGATC
GCTCCAAAGATCAGATAAATCTGAGTGCAGTGAATATTAAGTAATCATCAAAAGTATATGTTAAATTT
TATACTTTAGTAAGATGCTCTCTACAGGTGCTCTTTTCTTACTAAGCGGTTTCAGTTTCCAGCC
AGCCGAAAGAGGATATCAGTATATAAGAAAGCAATTCGGGGATGAAAGCTGACAGAGATTAACGA
GGACCACTTTTATTTGTTCTAGCAAGAAATTAACAGCACATACAGAGAGTCTACGATATCTT
TAAATAACATACATAATGCTCACTCAATTAATAATCGCTTCTGAAATACGACAGATCTTAGCATCTG
GGCAAGATTGCTGTTGTTGACTTTTGTGCCACATGGTGTGGCCATGTAATAATGATTTGCCCAATGA
TTGAAAAGTTTGCAGAACAAATTTCTGACGCTGCTTTTACAAATTTGATTTGATGAAAGTCTCAGATG
TTGCTCAAAAAGGTGAAGTTTCTTCCATCCCTACCTTAATCTTCTACAAGGGCGGTGAGGAGTTACCA
GAGTCTGCTGCTGCCAACCCAGCTGCTATCAAGCAAGCTATTGCTTCTTCCAAAGCTATAG

YGR209C, 104 aa (SEQ ID NO 188)

MYTQLKSASEYDSALAGSKLVVVDFPFWCQPKMIAPMIEKFAEQYSDAAPYKLVLDVDEVSVAQKAE
VSSMPTLIFYKGSKEVTRVVGVANPAIKQAIASNV

YHR039C-B, 1007 bp, exon1: 501-503, intron1: 504-665, exon2: 666-1007
(SEQ ID NO 197)

GTACATGCACCAATCTCGCTCAACTGCGTCAGATAGTTGTAGTCCCTCTTGACACATAAGCATTTCTGTTCTGT
GCTTGTGCTGCTCGGCTGTTTCAACGCTCACTCGATATATCTCTTCTAGGATCATGTGTTGACCTG

120/251

ACAAACAATGAGGCTCTGGAGCTTATGGAATTCGTGGCCAGAGTGTGTTTGTCCCGAAAAAACAATAAAGTA
AAATGACATACACAAATTTGGTCAAGTGTATGTTCAATACCATTCATTATGGTATGTCCTTGACCT
TTGTGAACTAGTGTCAACGTATTCGGCTGGATCATCACATAAGGCCCTCAACGTGTTGTGGCT
TTTTTCAATTTTCCCTTTCGCCCTATTAAGTCAAGTGTAGTGTGTTGGGCACTTACTCATACA
TCAATACATCTTAAGCATAACTAGTATACGGTATTTCAATGAGCATTTGGTAGGAATACCAAG
GTTTGTGTTGGGGCTCTGTTGGAGCATTAAGTGAATTTCAATCTATGTTGTAGCGTGTAGATCGAGGC
CCACCGTCATCTATACGACGCTCCAAATGAGAAAAACCAATTTGATTTGA

YLR414C, 263 aa (SEQ ID NO 294)

MRNFTLFFAIFSLGALILAIIVACAGSTKNYSPINKIYCAELDLQMKVSTVLPISLSATLSLGLPS
YINIGLSYCTVDSHNTQSSSPHIGINFNLSSLYVDINNNLEALMLDSVASVLPPEKLKSKMTYN
NLVKMPITILIGIVLTFVNLVFNVLWIHLPLTWFGAFSFPAPFAALLVSGSLGTTYSIKYILK
HNSYDVISISGRNYOGLMWAVVALLNFILMCSVRSRPTVIYANAPIEEKPLI

YMR251W-A, 680 bp, CDS: 501-680 (SEQ ID NO 317)

ATCCGTTGAAGCAACCGCATATGACATAAATGGTCTGGACATCTCCATGGCTGTGACTTGTGTGTAT
CTCACACTGTTAACGGCACCGTCTCGGAACGGTTCTCTCTGTGACAAATTTCTAGAACAGGGGCTACAG
TCTCGATAATAGAAATAAAGAGCATTTTGTGTAGCGCCGCCGCCGGCTTCCCAATAAGGAGGC
GCAGTTTATTCGGCGAGCTCTACTTCTCTCTATTTGGTAAAGCCCTTCTGTCTTCTGGCCAGTGGTGG
CTGACGCTGCGCCGAGAACATAGTATAGGATGTAATCTTTCGATGAGAGAAATTAGCAAGCGGAAA
AAACTATGCTAGCTAGCTAGTGTGTTTTCATCATATAAAGGAGAGAAATTTGTCTCACTATCTGAC
AGTTTCTGGGACGCTTAACTTTTATATGACAGAGCATATCAAAATCATACAGATATGTCAAAAAA
AAGACTAATAAATAAATGAATGTTATCTCAAGTGTGTTTCCGCCGTCCCTTCACTGGTTAGTAA
GTGCTCTAACAGTTCTTAACAGCTCAAGCTCAAGAAATGCTGCCCAACCAATTCGCCGTTTAAACAAG
GTAAAGTTGCAAGCGCCGCTGCTGTGCTAGCTGTGCTTGTGGCTTTTGTGATTTAA

YMR251W-A, 59 aa (SEQ ID NO 318)

MKLSQVVVSAVAFVFTGLVSAANSSNSSSSKAAQPIAGLNGKVAGAAAGVALAGALAFLLI

YNL030W, 812 bp, CDS: 501-812 (SEQ ID NO 323)

GTTTTCACACGAGCATAGCGCTGATTCGTGCTACATTTGGCGGATAATGAACGCTAAATGACCAACT
CCCATCGTAGAGCCCTTAGGGCTGCAATAGTTTACGGCTTAATGCGAAGTGTCTCGGAACGGA
CAACTGTGTCTGTCACCGGAAGTGTACTAGACCGAGATTTGCAATTTGTATGGCAGACGT
TCTGGAGCTTCTGCTCAAGCTTTTTCGGCGGCGAATGACAGCACCAACAAACAACACTGAC
AAGAAGCGTTTAAATTAATATGTTGTCACCTCGCCCTGGGCTGTTTATTCGGCTAGATACATAGC
TGTGTTGCGGTATGATGTAATCATATATAGTATATTAGGATGAGCGGTGAAGAGATTTTTTTTT
TTTCGCTTAAATTTATCTTTCTCTATCTTTTCTCTACATCTTGTTCAAAAGAGTAGCAAAAACA
ATCAATACAAATAAATATGTCGGTAGAGTTAAAGTTAGGTAAAGTCTAGGAAAAGTGTGCGCAAGC
GTCACAGAAAGATTCTAAGAGATAAATCAAGGTATCACTAAGCCAGCTATCAGAAGATTAGCTAGAA
GAGGTGTGTCAAGGTAATTTCTGTTTGTATCTACGAAGATCTAGAGCCGTCTTGAATCTTCTTGG
AATCCGTCATCAGGACCTCTGTACTTACACTGAACACGCAAGAGAAAGACTCTTACTTCTTGGATG
TTGTTTATGCTTTGAAGAGACAAAGGTAGAACCTTATATGTTTCTGGTGGTTAA

YNL030W, 103 aa (SEQ ID NO 324)

MSGRGKGKGLGKGAKRHKILRDNIOGTFKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRD
SVTYTEHAKRKTVTSLDVVYALKRQRTLYGFGG

YOL109W, 842 bp, CDS: 501-842 (SEQ ID NO 343)

CGAGGTCCTGCTTCACGAGCGGCTGTGCGCTAGTATTTGCCCGACGCTCGGGTGCCCTATCCCTAGAT
TTGCTGTCGCCGACCCAAATAGTATAAGTGTGGTTATGGTGTGACCGAGGCTTTATCGTGTTTA
TTCGTAGTGGGATTTGCTCCAGTGTATTTTGTATATCCAAATTAAGGTTTCTTACCTTAATTTAT
TTTATCATCTTTAGTTAATGCGTTTGTCTGTTTCTGCTGCTTCTGCGGTTCTCTCTCTCTCT
GTTTCTGTTGTTGCTTCCCAATGCGGATGCGCTATATGCGGTATATATGCGGTATAGGCTTTTACGT
CGAAGATCATCTGAGTTGCTGTATAGCCCTTCTACTTTTATCTTCTGTTTTHAACCATTTACTT
TAGTTTTTCTGATGCGGTTTCTCTGTATATTTAAAGTTTCAAAATGAGTCAAAAGAACATACAAAACTAC
GTTTATATCAATTAATAATGCTGAAAATTTCAAAAAGCTGAAAAGTCCGCCCCCAAGATGTCCACAAA

121/251

AGTTGGAAGAAACCAAGAAATCTTTGCAAAACAAAGGCCCAAGAAAGTAAAGGAACAAGCTGGAAGCTTCTA
TCGACAACTTAAAAATGAAGCTTACTCAGAAGCTGAACAGTGAAGGAAGGAAGAAACAATTTGCTG
ATGTTGTCACAAACAAAGAGACCGAAGCTGCCAACAAAGTTGAAGAAACAATAAGAACGAAGCTTCGCGG
CCGTAGTGAAGAGGAACCAACGAAGGAAGCGGTTTCTTGAAGAAATTTGAACCGTAAAAATTTGCTT
CCATTTTCAACTAA

YOL109W, 113 aa (SEQ ID NO 344)

MSEIQNKAEATAAQDVQOKLBETKESLQNKGOEVKEQAEASIDNLKNEATPEAEQVKKEQNIADGVEQK
KTEAANKVEETRKQASAAVSEKKETKKEGFLKKLNRIASIFN

YOR285W, 920 bp, CDS: 501-920 (SEQ ID NO 365)

ACTAGCAAGATGATCTGATATGTTGATTTATTTCCCTGTGCATTTGACTTTCAAAGATCATACAGCA
TACTAAGCCCTTTCTAGGAGACCTTCTGTGCAAAATATCAGAAATTTTCTTGATTTAAACGCGCATATA
TTGAGTATATGAAATTAACGGGACACTGTGTGAAAATTTCTAGTTGTACTTTTGTATATCCCTACGCT
GTAGACATATGAGCAATTAAGTATGCTTCCATAGTTGGCTTCCATAAGGCCCAATCCAGATATCACCTACGCT
ATGCTCTTTTCTTACTTGCATGCAATCAATTAATTTGATTTATCTTGGAACTTATTAAGTTACATCTG
ATTGCTTTTGTATTTTGTGGAGAAATTAATTTACCGCGGGGAAGTAAGGGGAGAAATTTTGTAG
GTGTATAAAGAGAGTGGAGCTTAATCAATCAAGAATTTCTTCTCTTTATTTTTCAGGTTTCTGAC
TAAGAAACCATATTAATAATGTGAAGCCCGTATGAATGCTTGGAAATGGAACCGGAGAGTCAAGTAAGA
ATGTTTCAATATTTCAATCTTACAGTTTGAAGACATCAAAAGAAATCGTTGGAAAGCATGATCTCTAATG
TGTGTTGTGTAGATTAGAAAGCCATCTGAGTACTCGATTTGTTGTTATATTTCTTCTTCCATCAATGTGC
CATATAGTCGCACTGAGCAATTTGCTTTAGATCTCTTTAGATTTTGAAGAAACAGATTTGGCATCCCAA
AACCTGACAGTCCAAAGAGCTAATTAATTTATGTGCTTCTGCAACGCGGGGAGAGCTCAAAAG
TGCCTCTCTCATGATGATTTCAACACCTCACTATATCTCGGCTCTATGAAATGATGTTGGTTTCTCATG
GGGTGATAAACTTGACTTATAG

YOR285W, 139 aa (SEQ ID NO 366)

MWKAVMNWNQTESQSKSNYSFEDMKRIUVGKHPNVVLDVREBSEYSIVHLPASINVPYRSH
DAFALDPLEFERQIGIPKPSAKELIPYCASGKRGEAQKVASSHGYSNTSLYPGSMNDWVSHGGDKLD
L

YOR327C, 848 bp, CDS: 501-848 (SEQ ID NO 369)

GTGTATTATTAATACCAACAATAAATAATATGCGCAATTTCTGTAGTAGTACTTACTATATTTGAA
TATTAAGGTTTTTCTGCTCTTACGTTATCTCTTTATCAGTCGTGGAACAAACCCACGGCGCTGTA
ACAAAGCACCATGAATCATTCAGTCGCCCTTAAAGCGCATTTCCACGGAGCGTTTATAGTATCTTTGCTC
ACATGATATACGGCTGACTTTTTTTTTTATTTTCTCTCTCTTCCGCAAAAGTGGCTCAAAAATTTCTT
CGGATTTTGGCATTTATAGCGGAATGTTGTCAGCGCAACCAACAAACACCAAGTTGTCGCACCCCAAGA
TGCAAAAGCGGGGAGCCAGTTAGTTTCTTCAAGTTTGTGTTGAAACAGCCCTTTAATATTTTATAGAA
AGGTAACATATCTGCTCAGTGAATAGTATCTGTAAGTCAGGCATACATCTCGAAACACTTCCAAATACAA
AATAAGAACCGCAACGATTCGTCATCAGTCCATAGCATTCATATGTCCTCCAGAGGAGAGTAACCT
CAGGCGCAAAACCAATTTCCCAAAACAAGACTGCTGCTTTGTAGACAAGAGATTTGATACACGCGTGGAA
TAATGAGAGATAATATCAACAAAGTTCGTAAGCGTGAAGGCTTAACATCTTGAAGGCAAAAGCTG
ATAACTTGGCTATCTCCGCAACAGGATTCAGAGAGCGCCCAACAGGGTCAGAAAGCAAAATGTGTGGGA
AAGATCTAAATAATGAGAATGTGTTATTTTCTAGTTGTTATTTTACTAGTGGTAAATTTATCTGTTCTTA
TCGTCGTCCTCATTTCACTAA

YOR327C, 115 aa (SEQ ID NO 370)

MSSSVYPDYPPPEESNGSNPNSQNKTAALRQEIDDTVGIMRDNINKVAERGLTSTIEDKADNLAI
AQGFRKANVRVQMKWKDLKMRCLFLVLIILLVLIIVPIVWHFS

YPL037C, 974 bp, CDS: 501-974 (SEQ ID NO 377)

TCACGGCTCTCTCTCTTTTTCGCAATATTTCTATTTTATCAATCGACTTCCCTTAATTTGCACTCGTACC
AAAAATGTTAAGCAGTATGCGGAAGAACGTGCGCGCTGAGTCTGAGTAAATGTTTGGGTCTCTTGAATGCG
ACTACGGTAGTAGTATGATGTTGCTCAACTTCAATATGTTTCACTTCTGATCCAAAGGAAGAGCGGTAT
GAAATTAATCTCTTGGCATGAGCGGCTAAGGGGACACCGCCCTTTTCTTCCGATGGGAATCAGGGTAA

126/251

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)

[illegible]

YGR146C 21aa public: 1..211 (SEQ ID NO 700)
MSTAFNDYCYVCDRLIPTSTQKNNINIRKLRQDNHETSSLSQNNLKYCEDCKLKDNPFLNEKLILSHLHK
KSRKTSHNLTPEPLSTYSKNLTASNLEPPTTSLSSPTTSSRTIPDELEKLESLISPLLPDGIYNPKQK
ENSPNSVDVEYDENIEHYLNLADSLRLDSSYQLHSAKALGYENNLPRSDMLIDDLHLSQGIINNNVNLMPFR
LSSS

YHR135C 211/bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)
 AAGGTATACGAGTACTACTATATAGAAAGTATAGCTAGAGCGAGGTCAAAACGCTGCAGCCGTTT
 AAGCAAGCTGCCCATGACTCTTTTGGGAGAGCACTGCTCATGACAGTACATGACATCTTCTACTCTGTACTGTTA
 TACGAGAAGAACCTCATAGATGTGATCTCTTAATGTGTACATACATACATCTTCTACTCTGTACTGTTA
 CATATGACTTTGACTTTACGATCTAATATATAATCCTTTGATGTATACCCGCTGTGGAGCTGTCTCT
 TTGCTTTCTTAACATTTTGTTCGCGGAAACAGAAAAACAGAACAAACAATATAGAGTGTGTACAT
 GGGTCTTTGATTTTGTGCTTCCTGCTGCAACAAAGCAAAACCTGTATATAGCTCTGTGACATG
 GTTTTATGTGGATGCCATGTAGAGAAAAGCACATACAAATTTTGGGCAATTGCTGGCCCTTTTC
 CAGCTCTCCCTCTCCCATCTATGCTACGCCATAGGAAATACATCTATGACATTAACCTCACACATA
 TTAACGGAACGCAATTTTATACGTAACAGAAACAAACATACCTACACAGAGCTGTGACGCGG
 CAAAGATCTTCGATGACCGCCACAGCAGCCGCGCAACTCCAACAGCAACTCTTCCAGAGATGACTTACTA
 TTGTCCGCCCTACATTACAAGTTGGGCAAAAATAAGGGGAGGTCTCTGTGTGTGTGTATATAGATTA
 CTATATATGATCAATTAAGGACCCGTGGATCAAAATTTGAGACGAGAAAAACGAGAGCCCTCTCAATTA
 GAGATATATATTAAGGCAATTAATTCGTGATGTCACATCCCAATATCCCTCAACGGTATCTACTTGGCC
 AAGAAGCTTTTGCACAAATATCTGTGTCAATTGATCTTTTGGGTGCCCTTTGGAAGTTATATGATATGCT
 GTGAGAGAAATTTTGTCTCAAAACGGTATGACCAAGTGTCTGTCTCAATATGTATATTTGATGTAAAGCT
 TTGACGACACATGACTGTGATATCGGTATACCAAGCAACGAACTTCTGATATGGAAGCCGCGCAAC
 CTACAGCGCAAAACATCATCTATTGTGATCGACTTTCGGTATGTGCAAAACAGTATGTGTATCCGAAAACCTMAAC

12/27/251

AGCAGATCCCATATGAGAGAAAGAAATCACTACGAGCGGCACCTCCAGATATGTCATTAATATCAACC
TTGGAGAGAGAGCATGTCACAGAAAGATGATATGAGAGCCCTGGGGTACAGTTTCTTTTATATTTCTTGAAG
TGCGAAGACCTCGGACAGGGTTATTAAGTCTCAAACATATGAAGCAAAAAATACGAAAGAATGTGGTAAAAAG
AAAGATCTACTAACTTTATACATCTACGTCACAGGCTACTCTGCAATATGAGAGGCTTATGAAATTCG
TCAGAAAGCTTTTCTTTGAAAGGTCTCCGATTTATGAGAGGCTTATGAAAACTATTTACTATCTGTAAATCG
ATGATTTTAGTGTAAACCGGACAGGCGATCATGATTTAGTTAGTAAATCGAATCGATGCGTGGTGGGATC
TTGCATATTAACAGAAAGCCAAATTTCTACAGGATAGGCCCATCCCAATCCACCAAGCAAAAAATGAGAA
AACATGAGAAACAACAGCTGCACACAGCTCAACAGCTCAACAGCTCCACACAGTCCACACAGCAGCAAC
AGCATATAGCTCTCAAAAACTGAGGCAAGATGTGGCAATTTCTCAATTTAAACAAGATTAGACCCCTATCT
CTTATAGACTTATACGATCTCAACCCACAGAAATACTGCAAGAACACAAACGAGACAGCAGCAAC
AAAACTTCAGAGAGCAACAATTCAGAGACCAACATTTGACAACGACAGCAGCAGCAACGACAGCACTC
GTGCAACAGGCAACCTTCATCTCAGCTTCACGTCACAGCAATCTCAATCTCAGAGCTTGGCGCTCGTTATC
AGCCACACCAACCACTCTGCGCTGCTTAAAGACTCTGTAAGCTCCGACCAATGACATTAATTCACAAAGTC
TAGCTGCTTCTCATTAAGGCGCTTTTCCAAAAATTTAGGTTCTTCTATA

YHR135C 538aa pulic: 1. 538 (SEQ ID NO 702)
MSMFI¹STL²LVN³LN⁴NGNANF⁵VOAK⁶OLH⁷QV⁸NDSP⁹ARSMT¹⁰ATTA¹¹NSNS¹²RD¹³ST¹⁴VG¹⁵L¹⁶HY
LK¹⁷KT¹⁸IG¹⁹DS²⁰FG²¹VE²²GT²³MT²⁴NG²⁵VP²⁶AI²⁷FP²⁸KT²⁹EA³⁰PL³¹RD³²BY³³TK³⁴YL³⁵NG³⁶PN³⁷IP³⁸Y³⁹AF⁴⁰GG⁴¹EL⁴²LN⁴³
K⁴⁴IG⁴⁵KT⁴⁶IG⁴⁷DS⁴⁸FG⁴⁹VE⁵⁰GT⁵¹MT⁵²NG⁵³VP⁵⁴AI⁵⁵FP⁵⁶KT⁵⁷EA⁵⁸PL⁵⁹RD⁶⁰BY⁶¹TK⁶²YL⁶³NG⁶⁴PN⁶⁵IP⁶⁶Y⁶⁷AF⁶⁸GG⁶⁹EL⁷⁰LN⁷¹
K⁷²IG⁷³KT⁷⁴IG⁷⁵DS⁷⁶FG⁷⁷VE⁷⁸GT⁷⁹MT⁸⁰NG⁸¹VP⁸²AI⁸³FP⁸⁴KT⁸⁵EA⁸⁶PL⁸⁷RD⁸⁸BY⁸⁹TK⁹⁰YL⁹¹NG⁹²PN⁹³IP⁹⁴Y⁹⁵AF⁹⁶GG⁹⁷EL⁹⁸LN⁹⁹
K¹⁰⁰IG¹⁰¹KT¹⁰²IG¹⁰³DS¹⁰⁴FG¹⁰⁵VE¹⁰⁶GT¹⁰⁷MT¹⁰⁸NG¹⁰⁹VP¹¹⁰AI¹¹¹FP¹¹²KT¹¹³EA¹¹⁴PL¹¹⁵RD¹¹⁶BY¹¹⁷TK¹¹⁸YL¹¹⁹NG¹²⁰PN¹²¹IP¹²²Y¹²³AF¹²⁴GG¹²⁵EL¹²⁶LN¹²⁷
K¹²⁸IG¹²⁹KT¹³⁰IG¹³¹DS¹³²FG¹³³VE¹³⁴GT¹³⁵MT¹³⁶NG¹³⁷VP¹³⁸AI¹³⁹FP¹⁴⁰KT¹⁴¹EA¹⁴²PL¹⁴³RD¹⁴⁴BY¹⁴⁵TK¹⁴⁶YL¹⁴⁷NG¹⁴⁸PN¹⁴⁹IP¹⁵⁰Y¹⁵¹AF¹⁵²GG¹⁵³EL¹⁵⁴LN¹⁵⁵
K¹⁵⁶IG¹⁵⁷KT¹⁵⁸IG¹⁵⁹DS¹⁶⁰FG¹⁶¹VE¹⁶²GT¹⁶³MT¹⁶⁴NG¹⁶⁵VP¹⁶⁶AI¹⁶⁷FP¹⁶⁸KT¹⁶⁹EA¹⁷⁰PL¹⁷¹RD¹⁷²BY¹⁷³TK¹⁷⁴YL¹⁷⁵NG¹⁷⁶PN¹⁷⁷IP¹⁷⁸Y¹⁷⁹AF¹⁸⁰GG¹⁸¹EL¹⁸²LN¹⁸³
K¹⁸⁴IG¹⁸⁵KT¹⁸⁶IG¹⁸⁷DS¹⁸⁸FG¹⁸⁹VE¹⁹⁰GT¹⁹¹MT¹⁹²NG¹⁹³VP¹⁹⁴AI¹⁹⁵FP¹⁹⁶KT¹⁹⁷EA¹⁹⁸PL¹⁹⁹RD²⁰⁰BY²⁰¹TK²⁰²YL²⁰³NG²⁰⁴PN²⁰⁵IP²⁰⁶Y²⁰⁷AF²⁰⁸GG²⁰⁹EL²¹⁰LN²¹¹
K²¹²IG²¹³KT²¹⁴IG²¹⁵DS²¹⁶FG²¹⁷VE²¹⁸GT²¹⁹MT²²⁰NG²²¹VP²²²AI²²³FP²²⁴KT²²⁵EA²²⁶PL²²⁷RD²²⁸BY²²⁹TK²³⁰YL²³¹NG²³²PN²³³IP²³⁴Y²³⁵AF²³⁶GG²³⁷EL²³⁸LN²³⁹
K²⁴⁰IG²⁴¹KT²⁴²IG²⁴³DS²⁴⁴FG²⁴⁵VE²⁴⁶GT²⁴⁷MT²⁴⁸NG²⁴⁹VP²⁵⁰AI²⁵¹FP²⁵²KT²⁵³EA²⁵⁴PL²⁵⁵RD²⁵⁶BY²⁵⁷TK²⁵⁸YL²⁵⁹NG²⁶⁰PN²⁶¹IP²⁶²Y²⁶³AF²⁶⁴GG²⁶⁵EL²⁶⁶LN²⁶⁷
K²⁶⁸IG²⁶⁹KT²⁷⁰IG²⁷¹DS²⁷²FG²⁷³VE²⁷⁴GT²⁷⁵MT²⁷⁶NG²⁷⁷VP²⁷⁸AI²⁷⁹FP²⁸⁰KT²⁸¹EA²⁸²PL²⁸³RD²⁸⁴BY²⁸⁵TK²⁸⁶YL²⁸⁷NG²⁸⁸PN²⁸⁹IP²⁹⁰Y²⁹¹AF²⁹²GG²⁹³EL²⁹⁴LN²⁹⁵
K²⁹⁶IG²⁹⁷KT²⁹⁸IG²⁹⁹DS³⁰⁰FG³⁰¹VE³⁰²GT³⁰³MT³⁰⁴NG³⁰⁵VP³⁰⁶AI³⁰⁷FP³⁰⁸KT³⁰⁹EA³¹⁰PL³¹¹RD³¹²BY³¹³TK³¹⁴YL³¹⁵NG³¹⁶PN³¹⁷IP³¹⁸Y³¹⁹AF³²⁰GG³²¹EL³²²LN³²³
K³²⁴IG³²⁵KT³²⁶IG³²⁷DS³²⁸FG³²⁹VE³³⁰GT³³¹MT³³²NG³³³VP³³⁴AI³³⁵FP³³⁶KT³³⁷EA³³⁸PL³³⁹RD³⁴⁰BY³⁴¹TK³⁴²YL³⁴³NG³⁴⁴PN³⁴⁵IP³⁴⁶Y³⁴⁷AF³⁴⁸GG³⁴⁹EL³⁵⁰LN³⁵¹
K³⁵²IG³⁵³KT³⁵⁴IG³⁵⁵DS³⁵⁶FG³⁵⁷VE³⁵⁸GT³⁵⁹MT³⁶⁰NG³⁶¹VP³⁶²AI³⁶³FP³⁶⁴KT³⁶⁵EA³⁶⁶PL³⁶⁷RD³⁶⁸BY³⁶⁹TK³⁷⁰YL³⁷¹NG³⁷²PN³⁷³IP³⁷⁴Y³⁷⁵AF³⁷⁶GG³⁷⁷EL³⁷⁸LN³⁷⁹
K³⁸⁰IG³⁸¹KT³⁸²IG³⁸³DS³⁸⁴FG³⁸⁵VE³⁸⁶GT³⁸⁷MT³⁸⁸NG³⁸⁹VP³⁹⁰AI³⁹¹FP³⁹²KT³⁹³EA³⁹⁴PL³⁹⁵RD³⁹⁶BY³⁹⁷TK³⁹⁸YL³⁹⁹NG⁴⁰⁰PN⁴⁰¹IP⁴⁰²Y⁴⁰³AF⁴⁰⁴GG⁴⁰⁵EL⁴⁰⁶LN⁴⁰⁷
K⁴⁰⁸IG⁴⁰⁹KT⁴¹⁰IG⁴¹¹DS⁴¹²FG⁴¹

YJL060W 1835BP CDS: 501..1835 public: 1..1835 (SEQ ID NO 703)

TAAGACGAGATGTTTTGAGTAGAGATTATGAAATCAACAGCTCATCTTTGATTCATAGCTCTTTAAAGATGT
AACGTAACTCTGTTTGATTAAGAGATCTTAATTCGAAGAGATTAAATTAATTTGTCAGGGTCTTAATAACT
ACGATGGCAATTTTCTGCGCCACAAGCTAACCTTTATGTAGTTCTTACGTAGTACAGAGGCG
TTGATATCACTTTTCTGGCCACAAGCTAACCTTTATGTAGTTCTTACGTAGTACAGAGGCG
CTGATGATGGGTATGCAATTAATGATATCTTTCTTCAATTAAGAACAAATCAACATCAATTAACAGCTATG
AGACAGTGACGTAAACATGTGCGTTTTTTTCTTCATTAATGAACAATCAACATCAATTAACAGCTATG
TTTAAAGAGGGAAGATCACTATAGATATTTATTAAGATGTTCATTAATTAATTCGATATAGATATCC
ATTGTTATCTTCTCTCATTAAGAACAAACAGATTCATATGTCATTAATTAATTAATTCGATATAGATATCC
CGAAATGTTGGCCACAATTAATTCATCTTCAACTTCGCAAGATGTTTGGCTGTACCAATATGAAC
CCGCTCGAAAGACGTGCCAATTCCTCAATCCAAACCAAGCCGGAACCTTACCATTCCTCAATGTGTATC
TTTCAATATCCCTCTCATTCATGTGCCATTAAGAGAGCTCAAGAACCTTACCATTCCTCAATGTGTATC
AATATTCCTCCACTAAGAGGTGAACCTTCAATTAATTAATTAATTCCTGATTAAGATGTATATTCCTATTATTA
ACACAGATATGGAACGGAAGAAATGTTACGCTAACACAGCTGCCAATGAAGTATATTCCTTCTTGGA
TGAGGCTTTTGAACGCTGGGGACGAGAGTATGTTTGTATTTGAACCTTTCTTGAACCAATATATCTTCAATA
TCGCAATCTTGCGGTGGTAAAGTTGTTATCGTCCCAATAATCTTCCAAAGAAATTTGATTCAAAGGAATTA
CTAAGAGTGAAGAAATGCAACATGCACTTGAAGCTTGAAGCTTGAAGAAATGTTTACAGCATTAACCAAGCAAGCTG
TCATATCAATCAACCTCTACACACCCATATGTAATTAAGTTTACAGCGGAGGAATTTAACCACTTTATAGTA
ACATTCCTGGTCAACGACCAACACTCTCTGATTAATTAAGTTTGAAGTATGACCACTTTATCTTCACTGATGT
CTTACTATGAGTATGCAACACTCTCTCAGAAATTTGGGCAACTAACTTTAACGGTGGTCTGCGCGGTA
AATCGTTTGGCTGATACGTGTTGGGAATTTGGTGGGCTTATCTTCAACAGGATGAGGATGGAATTTAAG
CAGTCAAGGCAATACAGAAATTTGTTTGTGATCTCCATCCCTCTACAGGAAGGTTGTTGAACCTTA
CAGTCAAGGCTTTAAATAATGGAATTTTGAATAAATGAACAGAGATATATCAACAAATTAATAAATTTT
TTACAGAACGTTTAAATAATGGAATTTTGAATAAATGAACAGAGATATATCAACAAATTAATAAATTTT
TCACATGATATTTTGAATTAATTTGGGACTACCATATACAGCTCGAAGAGGCTCATATTTTGTGCTCGTTGG
ATTCTCTTAAGTAAATAATCCGAGGCTATCTCCCTACCGAGAGATGTCGAATTAAGGAAATAAGTATCT
TTTGCATATTTCACTGTTGATTAATGAATTTAGGTGGTGGCATCTTCAACCATGATATCTATATCA
AAGGACGATTAAGAGGCTGCTAGATATTTAGGTGGTGGCATTTGAACAGATGATCTTATCTTGAATA
ATGCGGTAGAGAGATTTAAACTACTCAAGACTACTTTTAA

128/251

VJTI-060W 444aa public: 1..444 (SEO ID NO 704)

ATTTTATTACTCTCTCTCTTTTCCCTGTTTTCCTATTTTGTCTTTTGCATTTTGTCTTATGAGACATCAATAT
ATGCAAGTATGTTTATACATTTTATATTAATAATATGTAATATATAAATGCGATTTCTTACACATTAACCTCCAT
TCCTTTGTAAATCTCTCTCAATCTCTTTTCTTTTATCTTAAAGAGCCCTCCACAGCAACAGCTCAAT
TTTAATACGATTTTAAACATGAAGAATATCACAAAGTTTTCATTTCTGCCATCTGTCTCTCGCCCTCGCTA
TCAGGTTAATCTTCAAAAGCGATCCAGCACGAGTAAAGCTGCTCTGCTTTTGTCAGCTCAACAAATG
GTCAAGTAATCAATGCTCCGAGATCGTCTGCGATCTGTTGGTGGTCTTGTGGCCTCTTAAATAG

Y01.052C-A 61aa public: 1..61 (SEO ID NO 710)

YOL052C-A 61aa public: 1..61 (SEQ ID NO 710)

VKI.123W 8816n CDS: 501-881 public: 1..881 (SEO ID NO 705)

YOL099C 992bp CDS: 501..992 public: 1..992 (SEQ ID NO 711)
TGTCGCAATATGTGTATGCAATTTCTGTTTGCAGAGGGGACAACATCTCAATGAATGTATTTGTGGAAGGT
TGCAGATGTTACCAACACAGATCTGAAAATATGCCATGCAGAAATATTTTGTCAACATGTTGTGATTTCCA
ATAAAGAGGTTGTCCTTTGTGAGTGTCTATCAGACGTAAATTTGGAATTCAGTTTCAAGAAATGTTCTTGCAACAT
AAGGTTTCACCTTGATAGAGAGCTAGCATAGATGACCGAAATGTAGTAGTGAAGAACAGCAGAA
ATGGCTGAGTACATGACCTTCATTTACGCTTCTTCAACACAGAAACAGTGTGCGTATATATCTGCAATTC
AATAAATAGCAAAAGAGCAATGTCTCATTTTTCGAAATTTGGAATTTACGGATTTACGGCGCTCTTTC
ATTGATTTGATCGAGAAATATATATATATATATATATGATGACTTGGAAATCTCCATATATATTTATTTAG
AGTATTTAAGTGTGATGAGTGAACATATAGATAAAATATCTAAATACGACACTCTTGCATATATTTATGACATG
AGTTTGTGAAATTTGTCTGTGTTTACACCTAATCCACCGGTAACTGTCTTTTGTGGCAATCCGGTTAA
CTAATATTACTGTGTTAACGGTACTGAGCAGCGGTGTTTGTGAATTTGTCTTGGCAATGTATATAAAGG
TTTCAAAAATTTCTTGATCTGTGTGCTTGTAGGCTATTAATCCGATTCAGAAAACAGATGTGTCGTTTG
AAATTTGATGGAGATTTGCTATTCGCTCTGGGTTTTCGGAGAGGAGACTTGGAAAGTTTGGGAAGATCTTTTAG
GTAATGGCTCTTCCGAGATGATGATGTCTTCTTTCATAATTTACCTTTTGTGTTTCTTTCGCAACAGATTTCTTTCT
CTATTTTATTTGATATCGAATTAAGAAATTTTTCCTTGTGAGAACAGATTAACAATTTTGTCTCGTGGTTTTTTAT
CAGTGTCTCAAGAGAAATGCATTTGAA

RTLEINLLKNVKETEANLLARRIDRENKRHYEGFFINLRIHNIITFISEFFFN3IV

VOL099C 163aa public: 1..163 (SEO ID NO 712)

YOL099C 163aa public: 1.163 (SEQ ID NO 712)
 MKTLDKINYDLDFADFLKFPVFRNPTWTCFLGNPLTNLLVNGTGAACTFFECSLALIKVSKILL
 DLLLALLIDISENELCEPIDGDNWLCVFGFGEDLVGRSLGMAIPDDVDLLSITTFWFLCNSSSILFVF
 FLFLFLRTNLLLVFLVFLVKRNDL

CCAACAGCAGGAAACGAAGATGAGGCCCTCAATACTCTGACGAGGAAGAACCCACCGCC

VOL100W 3746bm CDS: 501 3746 public: 1 3746 (SEO ID NO 713)

TTAACGATTCGATCCGACCAATTTGTATGGTAATTAATTCGGTCCCTAGTTTAAACGACGGGAGAAATAGACGCCG
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CTACGTTTAGGCATCATCTTCAAGCTTCGCGCAACGACAAATTTATATTCACATCTTTAGTTTCTTAGCTGAGCGAGAGAA
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AAGGTATTTAGGGGTATTTAAGAACAGAGAACTACATAAATATGTTTGAAAGAGGAAACAAAGATTAAC
ATCTTGATGAACCCGAGAGCACTAATAGTTTAAAGAGCAAAATTAATATCTTCTCTCTCTCTCTCTTT
TTTTTCAATTTCCGCAAAATGTTATTTGATAGGATTTTCAATGAGCCCTTAGTTAGCCAGTTG
ATGACGAGAGACTAAACATTAATCTCTTAACGMAAAAGAGAAATCTTCGATTTAGACCCCATTAATG
ACGCAAAAGCCACTGCAGAAAGAGACATCCAGATAGAAAGCTTTGGCGATTTACTTTGGAAAAAAGAA
CCGCTTAGCCTTCAAAAGGCTTGAACGATACGGATAAATTTCAATTGAAATGTAACCATTAATCAGC
AGAGAAAAATTTGATGATGACACTTTTAAAGATAGTAATGATTAATGTAAGCAACGCGAATCTGTCG

1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784

YML028W 196aa public: 1..196 (SEQ ID NO 708)
MVAQVQKQAPLTKFKKAVDGVDFDEVSLDKYKGVWLAFTPLAFTFCPTETIIAFSEAAKKFFEEQGAQV
LFASTDSYSLAWLWNI PKREGGLGPGINTPLPLADYHSLSRDYLIEEGVALRGVLTIDPKGVIRHI
TITDI.PGVRNDFEALRLVAFVQDNDKNGTGLPCNMTPGAATIKPTVDEDSKEYFEAAKK

YOR052C-A 686bc CDS: 501 686 public: 1 686 (SEQ ID NO 709)

AGGATGATCAAGCCTATCTTCTCTTAGAGTAGGCCCAATGGGACCTTCTCTTTTAAAGAAA
AATACGGTCTATTAGACGAACCTGGCAGCATATTCTTCGCAAAATAATAGATGCCATAGACTACT
TACATTCGAACGGTATTATTCTATAGAGATATTAACACGAAAAATATCTTTTAGTAGGGAGAAATGAAGA
TCAAACTGACTGATTTTTCATCGGATTTACTGAAATCCATAATAATATAGCTTTCGAAACCCAGAT
ACGATTTATCAACAGGTCGAAATTTCTGGTTGGAACTCGCAATACGATCTCTCTTAACCTTTTAAATG

140/251

GTCCAGCATATTATATCATCCATAAAGCGTGTGGTGTGTGAAGACTGTCAACAATATCTTTATCCAAAT
CATAAACATTGAGAAACAATCTCCGATCTCAAGGTGATATGCTTATTAATAGCCCGATATTTCTTGAT
GTTGATATACCGGATATACAGTCATATATATGAACAATTAAGACAACTCCATATATAAATTTGCTACTCGT
TTCTGTGTATTAA

YIL074C_homolog 463aa (SEQ ID NO 438)

MSSPQQTIVNSFQALNLSCSNVASTSPQSFSLQVSPKPAKALPKFKTGDIKILLLLENNVQNTAINIP
KNQGYVEFYKSSLPEDELLEKKIDVHAIGIRSKTKLTKELIKAAKNLVIGTCFIGNQVDFLEFAAKS
GIAVNSPFFSNRSVAELVIAIITLARQLGDRSIELHTGWNKWSAKWELRGKTLGIVGIGHISQL
SVLAEMGNVIVYDVMTINSIGNSKVBSLDELKALDFVTHVPATPTGNKLLSLAPQFAAMKQAGYV
INASRGTVADI PALVQAMKAGIKAGALDVYHEPAKNGELFSDSLNEMASELCLSRNLVITPHIGGS
TEEAQSAIGIEVNSLTKYINBGA SQGVNFPFVSLRPLDLQNVVRVLYIHQNVPGVLKTVNNILSN
HNIEKQFSDSQGDIAYLADI SDVDISDQSLYEQLGQTPYKIATRLLY

YIR037W_homolog 486bp public: 1..486 (SEQ ID NO 439)

ATGCTCAATTTTACGAATTAGCTCCAAAGACGCCAAAGGTGAACCATATCCATTTGAACAATTTGAAA
GGGAAAGTTGTCTTATCGTCAATGTGCTTCCAAATGTGGATTCACTCTCCATACAGGGTTTGAAG
GAATTGAATTAAGAAATTTGCTGATCAACCACTACAAATCTTGGGTTTCCCATGTAAATCAATTTGGCCAC
CAAGAACCGAGTAGTAACGAAGAAATGGATCAATCTGTTCAATGAATCAAGGTGTACATTTCCCAAGTC
TTGGATAAATTTGAAGTCAATGGTGACAATACCGATCCAGTTTATAATATTTGAATCACAAAGAGT
GGTGTTTGGGATTCACCAAGATTAATAGGAATTTTGAATAATTTTGAATGACCAAAATGTTAAAGTT
ATTGAAAGATTGAGTTCATTGACTAGTCCGAGAAAGTATCGGTACCAAGATTGAAGAAATGTTGAAGAAA
TAA

YIR037W_homolog 161aa (SEQ ID NO 440)

MSQFYELAPDKAKGEPFPEQLKGVVLVUNVASKGFTPYQKGLLELNKKFADQPVQILPFCNQFGH
QEPGSEIEIGSFCSLNYGTFPVLDKIEVNDNDTPVYKYLKSKQSVGLGTRIKNWNEFKFLIDQNGKV
IERFSSLTSPESIGTKIEELLKX

YJR096W_homolog 849bp public: 1..849 (SEQ ID NO 441)

ATGTCATATCCGATTAATCAAACTCAATCCGGTCATACCATTCATCAATTCAGATTAGGATGTTATGAT
ATCCCAAGAAATAAACGGTTTCGGTAGTTTATGAAGCTTTGAAGTTGGATATCGTCATTTGTATCT
GCAGTTTATATGGAAGACGAAGAAGATCTTGAAGTTGATTAATTAATTTCTAGGAGAACCCCAAT
ATACCAGCATCTAGCTTTTATGACCAACCAAGCTTTGGAAATTAATTTGGGTACTTCAAGCACTAAA
CAAGCCATTCAACATATGCTCAAGTTGGTGATATAATAGATATATTTATTTATTTATGATTTCAT
TCTCATTTACCAAGTAAACCAACCTTTAGAAAGTGGAAAGTTTTCGAGGATCTGTGGAAAAAGGA
TGGATTAATAAATCAAGGTTTCTTAATTTAGTAACATCATATTAAGAAATTTGTGACATAAGCAAG
ATCCCTCCAGCTGTCATCAATTTGAATTTAGTCTTGGTGATGAGACAGGATTTAGCTACTTGGTGT
TTAAGTAAAGGTATCAATTTGAGGATATGACCATTAACCCATGGTAAACAAATTTACAAGTCAACAT
ACTGAAATTTCAAGAAATTAACCAAGATTAATAATCAGCTGCTCAATATTTGATTAATGGTCAATTA
CAAAAAGGTTATATACCATTAACCAAAACAACTCCATCTCGATTAAAGCAAAATCTTTCTTGTGTAT
GATTTTGAATTTGACTAATGAAGAAATTAAGGCTATTGATCAACCTGATGCTTATGAACCAACAGATTGG
GAATGTACTGATGCTCCATAG

YJR096W_homolog 282aa (SEQ ID NO 442)

MSYRLIKLNSGHTIPISIGLGYDIPRNKTVSVVYEACKVGYRHPDTAVLYGNEEVEIEGISKFLRNPIN
IPSEFPYTTKLWNQIGTSSTKQATSTWMAOVGDKLEYLDLLIHSPLPGKTRLESWKVLQDAVEKG
WIKNIGVNSYGNKHIEELLTNATIPPAVNIQIEISPMCHMRQDLATWCLSKGINVEAYAPITLHGNLQVNN
TEFQEIHQYKNKSAQILIKWLSQGYIPLPKTKTPSRLKENLSVDDFELTNEEIKAIIDQPDAYEPTDW
ECTDAP

YKL196C_homolog 603bp public: 1..603 (SEQ ID NO 443)

ATCAAGATTTATTACATTGTTATTTTAAGATCAAGTGGAGACAAGGCTTTAGAGTTTAACCTGCGACAGA
GATTTATCACAGTTTTCCTTTTCGAAAGAAATAGGGGTATCCCAATTCATGACTTTTGGCGACCAAC
GTATCCCAAGACATCAACTGACGACAGACAAGGTGTGAAGAGGTAATATATTTGCTCATCTATT
ACCAGATCAGAGGAATTTCTGATATCATTTATACGGACAAAGATATACCCTGTAAGACCAAGCATATACA
TTAAATGAAATTTTGAAGATATTTTATCATATGCTATCTTAAATCTGATTTGGGAAACATTTGAATAA
GCAATTCGAATCTTCAATATGACATATAGAACATATTTGAAAAATTAACAAGATCCCATCTGATGAT
GATTCATCATGAAAGTTCAACAAGAAATTAAGATGATTAAGGTTGTTTATACAAACATATTTGAAGGG
GTTTTCAAAGAGGAGAGAAATTAAGATTCATTTGGTTGACAAATCAGAGCATTTGTCAGGTTCTTCAAGA
ATGCTTTTATAAACACAGCAAGAAAACCAATTTCTTGTGTGTGATTAATGTA

141/251

YKL196C_homolog 200aa (SEQ ID NO 444)
MKIYVIGILRSSDKALELTSARDLSQSFPERNGVSQFTTFFAETVSPORTQPGQRQSVBEGNYIGHTY
TRSEGISGIIITDKDVPVPAYVTLINKILEYLSLHPKSDWENIDKANETKLOXGLEAYLKRYODPTQA
DSIMKVQQLDDTKVVLHKTIEBVLQRGEKLDLSLDKSEALSSSRMFYKQAKTKNSSCCVIM
TTCTGTGTATTAA

YKR076W_homolog 771bp public: 1..771 (SEQ ID NO 445)

ATGGATACAAAGGGGGGAGATTTCTTACAAAGGAGAAATTCAGACATTAATAAATGAAGACGACATTT
TCATTTAGGTACACTGACCATATATGATTTTCCCTCTTAGAGAAATTTGATCTTTAAGGCTGAACCA
GAATACGAGGAGATTTCAAGTTTCCAGTTTGGGACAAAAAAGAGTCAATCGTAAACAATGA
TCTGCTGAATCATCAGAAATTTGAATPACTGAATTCATATGATTTTGGCCAGTGAATATCCCGAAGTT
GATCTGTGTTCAAAAGCATTTAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT
AATGTTGTTTATAAAGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT
TTGGCAACCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT
GTTCAACACTTTAAGTGTATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT
TTATTTGATTTGAGATTTCTGCTTTTCCAGAACTACCAATTTTCCAGCACATCAAGTACCACATACAG
AAATCTCATATCAAGATTAATCATACGTTATACCAATTTGGGTCACGATACCAATATTTTACCATTG
GAAGAAAAGTAA

YKR076W_homolog 256aa (SEQ ID NO 446)

HDDKWRFPTEKELKTLKTEDDJSLGTPDHNYDFSLRELYFKAEPYEGRFTVPVLWDKKEGTIVNNE
SAEIIIRMLNTEFNNSILPSEVAEVDLVKPDLESQIDELNSWIYDINNNGVYKAGFASKEQVYAKEQNVF
DHLDKVLEALEKNKSGKEGFLNGQLTEADIRLYTTIIRFDPVYVQHPKCNIGTIRTHVPYIHNWLR
LLYWKIPGQETTFNEBHILKHYHTKSHIKINPVGITPLGPVPNLPLEEK

YKR092C_homolog 1287bp public: 1..1287 (SEQ ID NO 447)

ATGGGTGAGTGTGGTGGGAGGGAATATTAGCAGCAGGAGAAAGAGACCAAGATTCGTTGTTTT
GGGCTCATCTCTCTCTCTCTCTTACTACACAAAGAGAGTACGATTAAGTTTGGCCCAATGGG
TTGAAAAAATTTTAAATTTTCTTTTCTACCTCTTAAAGCTCAATATGATTTTCCAGAAAT
ATAGCAAGATGAGTTCATATCTCAAGATTTAGTTTGTAGTTTATATTAATGATTTTCCAGAAAT
GAAGAATTTGCAAGTTGAAGAGCATTTATCGAAATTTCTAGCAGGCAAGAAATTTACCAAAAGTTTCT
AAACAGTTGGAATTCATATTTGATGATGGAATCAAGAAAGAAACAAACCAAGAAATTCATCA
TCTGATAGTGAACACTTCTCATCTGAGTGAAGCTCCACTTCGGACAGCAAGCTCTCTCTCAGAT
ACGACAGCTCTCTCTCAGACAGTGAAGTTCTTCTCAGACAGTCAAGTTCTTCTCATCAGACAGTGAA
CAGACAGTACAGGAGAGCAACAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA
GAAACGAAATCTGGAAGAGCAACAAAGACAGCTGATTTCAAGTTCCAGTTCCGATCTCAAAA
TCTGATTCAGACTCAGACTCAGCTCCAGCTCTGATTTCAAGTTCTGATCTGATCTGATCTGATCTGAT
GACTCAGCTCAGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT
ACTGACAGTACCAATCTCTCAGAAAGTATCTGTAAGACAGCAAGATCATCTAGTATTCAGAAATCC
AAAGAGGACAAACAAACACAGACAGACAGACAGACAGACAGATGATATCAAGAGAAACCA
GTTAAAGATTTCAAAACGAGTCAAGATCATCTAGCATCATCTTCTACTGATTTCTCTGCAACTCCA
GAACAGAAATTAAGCCAGGCAAGAAACATTTTCTAGAAATAGATAGAAAGTAAAGTTAACTTTGAA
AATTCAGTATTAACAGCAATTTTACAGGAGCTGAGGAACTTCGGGAGAGAAAGGCTAGTGAAGAAA
TTATTACAAAGTCAAGGTAAGATTTTCAAGAAATTAATAAATGAAGAGAGAAAGTTTATAAAGGA
GGTAGTATCACTTTAGCTAGGCTCTCTATAAATTCGAAGATTAG

YKR092C_homolog 428aa (SEQ ID NO 448)

MGCEGMEGIFFSQKRRPRFVGLISLSYSHKRRATIKVCPNGLEKQFFNFHFFHLLKSLLQLLP
IAKMSNTQDLVLAYINDYVSRNBSLKLKALSFKLACKLPKVSQKLESIIDVENQEKSKPRNSS
SDSESSSESTDSSESSSESSSESSSESSSESSSESSSESSSESSSESSSESSSESSSESSSESS
ENKVEEDNKDTSDDSD
SUSDSDSDSE
EPFLKPGQRKHFSTRIDRSKNFENSVLQNTYKGAAGTWGEKASEKLQVRGKDFTKNKNKMRGSKYK
GSITLASGSYKFD

YLR043C_homolog 312bp public: 1..312 (SEQ ID NO 449)

ATGGTTTACGCTGTGCTACCTGAAGTAACTAAACCTTTCCAAACCTTTTAAAGGAAACAACTTATGTTT
GACTTTTTCGCCACTTGGTGGTCCATTAATGATGATCTCTCCATTTATAGAAAAATTTCCAAAACTGA
TATCTTAATTAATAATTTTGAAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT
AGTTCTATGCCAACTTTGATTTTATTTCAAAAATGTTGAAGAGTCAATCGTGTCTATTTGGTCTAAACCA
GCTGCTATTAAACAGCTTTGCTTCTCTCTTAA

146/251

YPL190C_homolog 396bp public: 1..396 (Seq ID NO 463)

ATGCCAAGTACAAAGAATCATCTCTACTCTGAGTATCTCCATTAAGACTCTTAAAAAGAAAGTCAACTA
GATTATGTGATCAATCTCAACCATGACAGATTAATGTATGTAATTAATCAACCAATCAATTAATGAAGAA
ATTTTATGTGCATTAATTTGACATCTAATTTTTCGATATGTGAATATCAATTTCTTAATCTCAATAGAT
GGTTTATGCTTCAATTAATTTAGTAATTTTAATACGCGTCAATGTGGCGTGAATTAATTTGAAATATCAA
CAAAATCTCAAGATGAACACACTGTGATATTAATGCTGTCAAGAAATCTTAAGCTAATTTTCTCAGAGAAA
CAAAATCTCAAGATGAACACACTGTGATATTAATGCTGTCAAGAAATCTTAAGCTAATTTTCTCAGAGAAA

YPL190C_homolog_131aa (SEQ ID NO 464)
MPSTRSSSTEYSHDSSKKVKLDYVLNKKPQTLVKKNLTKINKILLHLVLLFSAFGDIISINLQN
GFAFTFSNLNSATLALRNLLKODFFDKPLVINYAVKEKASIQEKQLQDENDEVMPSYE

YBR112C_homolog 3243bp public: 1..3243(SEQ ID NO 465)

identificando o nome do usuário e o endereço IP. O sistema de autenticação é baseado em um protocolo de troca de chaves de sessão, onde o cliente e o servidor trocam informações para gerar uma chave única para a sessão. O sistema também utiliza um mecanismo de autenticação de dois fatores, onde o usuário precisa fornecer uma senha e um código de verificação gerado por um aplicativo de autenticação. O sistema de autenticação é projetado para ser seguro e resistente a ataques de força bruta e ataques de phishing. O sistema também possui um mecanismo de recuperação de senha, onde o usuário pode solicitar uma nova senha se esquecer a atual. O sistema de autenticação é integrado ao sistema de controle de acesso, permitindo que apenas usuários autenticados possam acessar os recursos do sistema. O sistema de autenticação é projetado para ser escalável e capaz de suportar um grande número de usuários simultâneos. O sistema de autenticação é projetado para ser fácil de usar e não interferir com a produtividade do usuário. O sistema de autenticação é projetado para ser seguro e resistente a ataques de força bruta e ataques de phishing. O sistema também possui um mecanismo de recuperação de senha, onde o usuário pode solicitar uma nova senha se esquecer a atual. O sistema de autenticação é integrado ao sistema de controle de acesso, permitindo que apenas usuários autenticados possam acessar os recursos do sistema. O sistema de autenticação é projetado para ser escalável e capaz de suportar um grande número de usuários simultâneos. O sistema de autenticação é projetado para ser fácil de usar e não interferir com a produtividade do usuário.

YBR112C_homopg1080aa (Seq ID NO 4566)
 MYATHNTIKQ0000000000RRPRLPENGSLHSLDASGSLAESGIDIERAATNSALRHSPNNEDILVKI
 QAVQ0RAAQ0000000000RPSLSALNETTVSTYLAAGLSAESGIDIERAATNSALRHSPNNEDILVKI
 TSNVSKQFLAEALTEYALNPHNENGTWELDLCHCYLMNLDRAYAYQALRYFLYENPVKILHNG
 IGILYXDRGSLAEAYEARVLDLPNPFKATNIFRLGIYKHQ00PALCEFLYIILNRPRLYLP
 DWDFIGSYTEEDQKMGNCAKAYEYVLQNPHHAYTQDGLCSQAEKNSPANGAAAPHPHPODL
 TALKVYLKQSLSEVDSDSHAWSLYGLRIVETNDFRDLAYEAPQQAENLDNNRPHTKARLEUTIKLQDGN
 DALDAYTRAIRLNTPISEWMDGLIYECNNQDILSALDAYEAPQQAENLDNNRPHTKARLEUTIKLQDGN
 THPPQRPSPSQPRLPQGVWLESTQ0000000000PPRQ00000LOH00000PQ00000PQ00000
 VSLPPQIQLPQAKPRLVNDQ00STPRLHMLAQPGQ0PQLPRLPHN000PQ0I0KRPQ0E0B0
 SYPPEPQI00000000PRLPHN000STPRLHMLAQPGQ0PQLPRLPHN000PQ0I0KRPQ0E0B0
 ASQYQPPQ00YQ0HIALVROE0VNVHYSIAPETRTPIQLNPNMESTTTPYQLKKEEKPEKPAIT
 VSAPEPAKTVDDQVITQESALAAAAAASAPASAPGIDIKTTPVSTTPATSTTALDAPVSVQ0VGA0
 INVQ0EKVQEDQI0Y0QVKEPVESQ0EVTPALPAPALATAPPEAPTDKDVYMAPEKSNTPVQSYIYE
 QNTRVSEAKRAEENSGKDLKEDNDEKELIKRPVETTESPVVQPVKEENKEVVEVPSPEQ0TSERK
 EVKNGSITKKRPLEENKVDI0PSSNITPA0NEAKSGEELKQTTTTPAKQ0EVEVEVPSSTETVSKRP
 DEVDK0NKEKQEDKEDVMADEDVQK0DENPPEPKRIEEDENTDDE

YDR145W homolog 1536bp public: 1..1536(SEQ ID NO 467)

[illegible][illegible]

YDR154C_homolog_33bp public: 1..333 (SEQ ID NO 469)
ATCATGCTGCTCAAAACAGCTGCTCAAAATTCACAGAGGCTTATATGCTGTGGTAAAAAGTTTGGTTACA
AAGGTCATATTTTCCACAGATCTACCATCCATCTTATCAGCTGATGAGTTTACCAACTTAAACG
GTACTGTGTGTTAAAGTATTTACGTGACCAAAATTGGCATGAAACCTTGTCTCAAGACATGACAGC
CAGGTGTTTCTATATGCGCAATCTGCTGCTCAAAACCATAGTCTCCCATTTCTTACATACACGCTTC
CATCCCATGTGTGATGCTCAAAACAGCTGTATTTTCCGGGAAGTACTGATGAGTTTAC

YDR154C_homolog_110aa (SEQ ID NO 470)
MMSQRRSSKISELIVYAKKLVLTIVLSTESHNSHSCFNVISPTLVSVKVFYVPIILSKTKLSRDMD
QVCCLMPSIVTQPMVNPNSLPPFAHGMNNTLPSVSSMW

YDR342C_homolog 550aa (SEQ ID NO 476) 150/251

[illegible]

YDR343C_homolog 1641bp public: 1..1641(SEQ ID NO 477)

[illegible]

YDR343C_homolog 546aa (SEQ ID NO 478)

120323Z 120615Z
MODDANVSST12A61VNNELIKVNDKDFROBEQWNTL2KRPXVAIYGLIMMCL1ANGGVEFFGPDGTS12
PIMSOP1LEBRRGQKAGCGLYFNSVRKOTLMTGLNNAQCAIALPLSKVGDGKRGVRVIMTAYIYVGLI
IYV1A0SHAWYQW01GAILGTLVANGM1SVLCPLP1SEVSPHAKG1YVOCQ0LMTGLTGLIYGYCTTGTGT
KVSJSDS0001PCL2C3AMALC1AGKAWRMPESRVSIVK00T0R0DANAK3ATKVNKSEDPALNRELO0
1QAGVEBRL1AGRASW0T1ENGRKIFRFRVYVWGL0AL00T0R0DANAFST1FLFKSGVSD0T0S12
1ICV1NPASTFVGTIY1AERMRRC1CL1LTSYVAM5VCP1YSLVNG0H0Y1XIDPGASRKP0DAN1FMTI
SL1VEFFFAVWAGVAGV1ISL1YELKRSKVMGLMANMTWGL1SFTSFTIDA1HRYVGYVMGCCL
VTS1VEFFFAVWYERKGLTLEIDELYSKTVLPMK5AGVWPPSEEMMA1STG1AGAKREBEHV

YDR544C_homolog 1700bp (SEQ ID NO 479)

[illegible]

WO 02/064766

151/251

GCTCTTTTCCACAAATTTACCTGCTGCTCCCAATTCCTGGAGAATTCGGTAAATGGCTGCA
 TTAGCAACCTACAGACAGGGGTCATTTGTTGGTAAATGAATTTTCAACACAGAAACCTTG
 GCATCACCCTTCGGATTTAGCTCTTCTCATTCTGAAATGATCAATGCGACCTTTTAAAGAT
 GGACAGTTGATTTAAATACAAAGTAATTTGGGAAGTGGCTTCAATTATTAATGTTAACT
 TCCGATCCACTTTGTGTCACATATCTCAATTAATGTTGCTGAATAGACCTCGTACAAAGCT
 TTTATTTAGAGATTTAGCTCAAAACAGTAAATTAAGTGAACCCAACTTCAATTAAGCTTAA
 ACTCTGTGGGGTTAAATTTCTTTGAAACCAACAGGTACCGAGTAAATTTCAACAA
 ATATGGAATTTTGAACCTCATCAGTCAAACTTTGATGTTGATGCTTGCATTCGTCAACTACACCT
 TTGGTAATTCGAATAATTTGTGTCCTCTGTAAGCTTTGATTAAGCATTAAGCATTAAGCAACAT
 GCTTCTCTCAAGCCTTCAAGTGGTTTATTAAGAAGAAAACAATTAACATGAGATAT
 CCACAGTCCCTCGCATGTGAATGCTGTAAGACCGTTTGTAAGCTAAGATTTATGACTATATGGA
 TTGGGTTCCGAACATGAGCTGTGGTGGCAATTAATAATTCGAATTAAGATCCACAACTC
 AAGCTATGTAGTAATGTAACGTGAATGCGGAAGAATCTCTAAGCTTTAGAAATTTTGGATT
 AACGGTAATTAATGTGTCATCTTTAAGTATCTTTTGAATAGTACCTTCCTCTGTTGAAT
 TCAAAAAAAAAAAAAACGTGA

YDR544C_homolog 548aa (SEQ ID NO 480)

[illegible]

YEL071W_homolog 1584bp public: 1..1584(SEQ ID NO 481)

1250712612605632 2353632 3353632
 ATGCAAGAGGATATTTAGTACAGATCTGCTTGTGATTTTGTATTTGACGAAACAACGTGGCATATGATTTACGT
 CGTTATATATATGTTTGGTCCGCTGGCATCTTTATTTATTTATCAAAACAAGTCCTTTTATCCGACGAGATATTTATCC
 CAABAAGTCCACGTGATGCGAATAATTCACAGCACTTGAAATTCACAAATCTGATATTTATTTAAATGTTA
 TTACCTGAGATATTCATATTTATCTATGTAAAGACAGACTTATTTGTTTTTCAACGAAAGTGGATGTGAAG
 TTATAGAGGTCATACACATAGCTTTGTATCCACAGGGTGGGAACAACGACGCAAGTGGCTTTATCTATCTATATGAATAT
 TGTATATGATBACAAGTACGTGTTGTATCCACAGGGTGGGAACAACGACGCAAGTGGCTTTATCTATCTATATGAATATCA
 ATTTATTAAGTGCAGCGTGGTGTATTTTGTGGAACAAGTGTATCAAGTATATGATTTGCTGTACAGAGGGCTATTT
 TTCCCGCTGCACTTTGGAGCTTAAAGGTCGTGTTCAGTGTGTCTGTTTAAAGTTTGAAGCTGTCTTGTCCGACGCGT
 TTCCGCTTGTATGATACGGTATGATACAGTGTGTCTGTTTAAAGTTTGAAGCTGTCTTGTCCGACGCGT
 TACGTTTATATCTCTGTTGATATTTATATACGTGTGTTCGATTTCTATGTGTCATATGAACAGTGTGTTTAT
 GAGTATGCAAGGTACTTTGGGATATTTATATACGTGTGTTCGATTTCTATGTGTCATATGAACAGTGTGTTTAT
 AATGTGGCATTTTATAGCTGTATGATATATGAGAGCCGCTTCAAAAAGTTTGTTCACAGCTTATGAAGAAG
 TTGCAAGAAATTTTATTCGCTTTTGTGAATTCATGGAACAATCTCACAAAAAGTGTACGTATGACATATTTA
 GGTGTGGAGCAACCTTATGGAAGAGCGTGACTTCCCATCTATATGTGTTTATATGGAACCTCTGGCTCTCAAC
 AAGAGTACGACACAGAAATATGGAACAATCTCTGTGGGATATGCAATGAAAGAAAGTTTATGTACACAT
 GGGATTTATTTSCACAAAGATGAGGCTCAAAATACATATCATATATGTGTCATGGAAGATATTCATCCCTATGAC
 ACACATCTTGAAGCGCGGTGTTTTACAAATATGATACGTTTCTATTTCCATTTGGCAGATCTTTACGGGTATGTT
 GAGGACATCAATTCACAGTTAATATGATGTCGATCCGACGTTGACAGATATGATATCAAAATCTTGCTT
 GCTGACATTTGGGTTATGTGTCATTTGAGATGGGAATTTACACTTGAACGTTTCTGTGAAAGATATTTCT
 CTCGAAATTTGAATTAATCTATTCGAAACAATTTGTCTATTAATATGATATGATCTACATTTTCT
 GCTGATACATTTGGTTGGATTTTCCAAAGCAATTAATCAATATGAGTATCTCAAGAAATGAAATATGAGTCTCAA
 TTATATCAAAAGATTCAAACAACATTTACGATTCCAAATGGAATCATGAACCCATATTAATATACGTTTAT

YEL071W_homolog 527aa(SEQ ID NO 482)

12407-14-140625-2
 MORUWATASILLIRANVACRFSYINGELPIVASYSTKIVPPFIADIVISQKQORDARFKELOSODIEKFXFV
 LPESSITIDEDDLFREFEDMWRKQKQSOVLAKRETHREQVASILIKYINDNKLAVFPGQGNAGVLUGGNSNP
 IPBETIISLAMDNIISFDPISGILKIDAGVILETAQVIAQEGYIEPLDIDGAGSGVGGVAGNACAGGAGG
 LRLRIYSGSLHGSVGLAEVLEPDGVIVNMSHSLRNDGMDGYDKQGFISSEBGNLGIITGVSIILCPSPRPOAQ

161/251

ACTTTTGGTACTGGTATGCTGCTTAT
ATTATTTCAAAACTTTGGAAAGCTTAA

YCR009C homolog 293aa (SEQ ID NO 524)

YDR178w_homolog 169aa (SEQ ID NO 530)
MISTYRIGLTLTKSSSSSTTTVRLLLANTRGKTTTPQPGYIVGTVNDAYVPPPHKLGLSLH
WTSRIVAIGMLPLVLAFFPTGCGGADLTMTSMALLFCHCTGFGSCIIDDIPKRVGSGYHNYAMVLL
TFGSGIAGYQIETREKGVSNISKLWKA

YDR202C homolog 387bp CDS: 1..>387 public: 1..387 (SEQ ID NO 531)

GATTAAGAAATTCATATGGTATATTAATAATTAATTTTACCCGATTTACTCAATCATAGAGACTTTTA
 CAGATTTCTTCAAATTTCTGTGATGATACAAATTCACCACAAGAACCTGATTCCAAACAATGTATTTCGAAAAA
 GGTCACATATCATAGTACCTTTGTCTTTTAAACCAATCAACAAGATTTCTGTCAAATGGGATTAATAACCCGA
 TATGCCATATCATACAGATCTTAAATTTGACGGTTAAAGCAATTTATTTCAACAAGCATTTTCCATTAAG
 TTGCGCTTAATATACAGCCCAATGGTTTATTTAGAGCAACATTTGTTAAT

YDR202C homolog 129aa (SEQ ID NO 532)

YDR202C_homolog_129aa (SEQ ID NO 532)
MTANILNNKTFIDTVLSIGSTQNDKELHWYIINILPDLPOIETLQICSNLWYNSPQEPDSKQCIK
GSKIPIPISTWQODSVNGITTRDGPVITDNLTKVNHVFNKHFHKLRLIKPMVLEOLVN

VDR256C homolog 1458bp public: 1..1458(SEO ID NO 533)

[illegible][illegible]

TTAGCTGGATCTAACCCAGATTACGCCCCAGAGAGATTGTGTTCAAGAACATTGCTGCTGGTAACTACCCCA
TTAGTGAACTGGCTTACTTCAACACCATGACTACCGCCAGAGCTAATGAAGCTGAAATTTCTGTGTTTGAT
TTGACCAATGCTTTGGCCATCCAGAGAAATCCACTGAGAGAAATTTGGTAAGTTCTACTTTGATGAAGAAC
CCAAAGAACTACTTTGCTGTAAGTTGAACAAGCTGCTTCTCTCCAGCCCACTGTTCTCTTACATGAA
CCATCTGCTGATCATGCTTGCATCAAGATTGTTCTCTATGCTGTATATCTTCAACACACAGATATGGGT
ACCAATCTGATCAAAATCCCACTGAAGCTGCTGTCACCGGTGTTTCTCAACCCACATATGAGAGAT
GGTGCTATGACTGTTTAAATGGTAACTTTGGGTAGCCATCCAAACTACTTGGCCAGTGAATAGCCCAATTCAA
TTTAAACAAATTTTCTTCTCAAGAGACCAAGTATGGAAATGGTGTGCCACTCCATTTCTCACTGGHAA
GCCACCCAGCTGTTTCCAAACAAGCTCAAGAAATGTGGAAAGTGTGAAGAGATATCCAAACCAACCA
GAACATTTTGGCCCCAACAACTTGTCTATCAATGCTGCTGTGCTGCTATCTCCAGAGACAGAGTGTTT
GACATATCTTTGTAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAANGGAAGTTTGTGGAAATTTATCTCCA
AGAAAAATAA

CCAAGAACTACTTCTGGCTGAAAGTTGGAACAAGCTGCTTTCTCTCCAGCCACACAGTGTCTTACATGAA
 TACTTGTGTCATCGACTTGCATCAAGATTTCTTCCATGCTGTATCTCAACACACAGATATGGGT
 ACCAACTATCTCAAACTCCCACTGAAGCTTGCTTCACCGTGTGTTTCAACCCACATATCAGAGAT
 GGTCGTATGACTGTTTAATGTGTAACCTTGGGTAGCCATCCAACTACTTGGCCAGTGAATAGCCCAAGTTGAA
 TTAAACAACTTTCTTCTTCAAGAGACCAAGAAAGTTGGAATGTGCTGCTCACTCATCTTCTGGAA
 GCCACCCAGCTGTTTTCAAACAAGCTCAAGAATTTGTGGAAGTGTGAAGAGATATCCAAACCAACAA
 GAACATTTTGGCCCCAACAACTTGTCTGTACATGCTGCTGTGCTGCTATCTCAAGACACAGAGTGTGT
 GATCATTTTGTGTAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTTTGGAAATTATCTCCA
 AGAAAAATA

YDR256C_homolog 485aa (SEQ ID NO 534)

YDR256C_homolog 485aa (SEQ ID NO 534)
MAPTINNSNGQIPTEPPFATQVQGHGQLLQDFNLIDSLAHFDRKIPERVVHAKSGAYGVFEVTDI
TDICAAFLDTVGKKITLFTSTFVGGELSGADTADPRGFATKVTBEGNLDLVNNTPVFFITRDSK
PPHIIHQKRNPETHLKOANFMFDWLYTNSESIHOVMVLFSDRGTPASTVREMNNGYSCHTYKVNKKGEW
LYQVQHITSDQIGITLTNEEALGASPNFYEQOAFSPHATVYMEPSADPVLQSLRFSVADTHRHRLG
LTKVPHKKYPLRFGKGTILNENPKAYEVDQAFSPHATVYMEPSADPVLQSLRFSVADTHRHRLG
TNYTQIPVNCPTGAVFNPHRDGAMTNGNLGSHPNYLASKPVFEKQFSIQEDQVWNGAATPFPHWK
ATPADFFKQAQELWKVLYKRYPNQQLAHNIAVHAAGADAIIQDRFYAFGKVSQDLADAIKKEVLELSP
RK

VER103W_homolog 1971bp public: 1..1971 (SEQ ID NO 535)

[illegible]

170/251

YPR035w_homolog_373aa(SEQ ID NO 570)

MTSLSTLEGTALLAKLYELSSONGKILAEYWIADLEGTRSKRTLSSKPPISVDLPEMNNYDGSSTGQAFG
HSDVYLVPVAPYPPDFRGKDNILVINECANGDTPNFKPHRECKLIMAHASSEWFGQLEETLDD
CYDDYVGMPPKGSFPAPGCGFVCGVGVYARVITAEHYAACYAGINISAEVWQSQEFOVGPCE
GIEDDQMLATILDRVAEEPAVKTSPIHKPKLPGMNNAGCHTWNSTKSMRYVGGKAVIESALSLLAK
RKHEMLLYGANDDQULTGHHEGHNDTSSGVANNGASIRITRQVAKEGYSITFEDRRPASNIDYLVLT
GIMVETIGSIIEDDQULTGHHEGHNDTSSGVANNGASIRITRQVAKEGYSITFEDRRPASNIDYLVLT

YMR099C_homolog 900bp public: 1..900(SEQ ID NO 571)

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YMR099C_homo1og 299aa (SEQ ID NO 572)

MEVELEEDRVITITDENDSTNRATILKEGARVYVSMKNNQEKMLMBEBAHIDGSAVBGGIILPVFOCK
QDSNHPTEKLPQHGABNSTWELGCTOSPITVFOGLEPENVDPTEKLMAYDPYILTVSLTXDKL
VNSIDVENTGKEAEPFEMNLPHYTYRIHDITDLYTNLIDQOCIDQLGESITIEKAPVTSFHEEDRIAS
KXSLERSIQVNGQVULFNLRHXYLPSVWVNNPWTKABEGMAFQPKSGFHQMCVBEGRHNSWVSLPA
GGRMSGDEITITGEGEIKVQANTY

YB1.085W homolog 3519bp public: 1..3519(SEQ ID NO 573)

[illegible]

WO 02/064766

PCT/EP01/15398

171/251

YBL085W homolog 1172aa (SEQ ID NO 574)

[illegible]

YBR019C_homolog 2028bp public: 1..2028(SEQ ID NO 575)

[illegible]

17/4/251
YI1057C_homolog 201aa (SEQ ID NO 584)
MAGKKRSSEALPLDLDNIKPMDHLOPVPPTRSSSTISIESADBPGRKOVLLPPTIKEDLEFORESF
VRDWMNDPFTGHLHYTPPVKMSCCNNLEKIKPTMNKNSKFRPDLQHHIDKLIKDEKCCGYE
LNFKEGEVEIDNKTWKDETDHGFSEEDMYDRHMRLELDVSCNSESAMVDEVYSKIPM

YKR097W_homolog 1662bp public: 1..1662 (SEQ ID NO 585)
ATGCGCTCTCCACTGCTGTGTGAATCTTCAATTCGAGAGCTCCACCACTATCAATTCACCTCAA
GACCATGAGTCCAAAAGTGTCTCTTAATACGACACTGTGTATGACAGCAATGCTCACCTCAAC
TTACATCAAGATGTTGTTATATGAAAAGATGACTATCTATCTACTAGTGTCTTTAATGCTTACTCT
GGTAAACAAAACCGGTGATGCTCCAAAGACAGAAATGTCAGATATCCACTCTCCATACAACTT
TGGTGGGGTCCAGATATTAACAAGATGTTGTGTGAAGTATGCTGTGTGTGTGTGTGTGTGTGT
TACTGTGAATATCTGT
AAGGTGAATTTAAAAAAGT
AATCCACATTAAGGT
TTGGGTGACGAATATGCTGT
AAACACAAAGTTTGT
TTTGT
GAACATGT
TCTGT
GACCATATCACCAGT
ATTGATTTATTTCCACTGT
ACATGT
ATTGT
GCATGT
TCCGAATACATATCCAAAGT
AAGAGATGATCATGTGAATATACCAAGAGCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GAATACGAAGAAAGT
TTGAACCCCAATTAAGT
AAGTTGT
GCATTA

YKR097W_homolog 553aa (SEQ ID NO 586)
MAPTRAVESINFGSHPIKSTQDPLVOKLSINTDVTIVIRHNADEPPLUYEDLLKETTISTGALMYS
GNKTRGSPKRXIYDESTRSHNIMDPVKNQVDELTKISRSRALDYLRREKLEFVDAVAGWDRYH
KRIILCARAHALFWTNMLIPTEBELNKFGEPTIYNAGORPANHITGNTSATSVEINFKDMENYI
LGTEVAGEENKGIPTVMEYLPPIRKHVLTSHSSCNGVEGDVTLTFGLSGTKTISADPQRKLGSD
EHCEWSNGVYNIPEGCVAKCLDLSAEKEPEIENSIFGAILENVVDPPIKVVYEDSSITENTRCAIP
IDFIPSAKITCLADHPNIIILITCDASGVLPEVSKLJNANOVWHPISGYSKMAEGEVEPTQATFS
ACEGQFLVLPKRYAQLSDKISHNANAMLNTSMVSSVAQGGKRCPLKTRAILDAIHSGLSKY
EYKGVFVNINVPISCPGVSEILNPTKAMTGTDSFNKEIKSLATKFAENFKTYADATAEVKAAPR
A

YOL126C_homolog 1014bp public: 1..1014 (SEQ ID NO 587)
ATGCTCAAGCTCGCTATTTTGGAGCTGCGTGGGATTTGTGCAACCATTAATCTTATTTGACCAATTA
AACCAATATTTGATGAATTTGCAATTTATTTGATGTCTCATATGTCAGAGTGTGTGTGATTTATCT
CANATCAATTTGATTAATCACTCATATTAATTTGCAAAAGATTAAGAAATTAACCTGCATTAAGCT
GATGATTTAAAGGTTCTGATTTAGCATTAATCCAGCTGTGTCCAAAGTGTGTGTGTGTGTGTGTGT
CAGATATTTCAATTAATTAATCATATTCATTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
AAGCTTTGT
GCTAAAGGT
TTTATTTCTCAATTAATTTCTGATGCAATTAACCATTTGATTTCAATTAATTTGATTTATTTGAA
TTCGTGTAAACCATTTGCTCATTAATTTCTATTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GAACAAAAGAAAGATTAATCAAAAGATTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GCTGTGTCCGCACTTTATTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
AATGTGTAAACGATATTTGT
GCTAAGAAATTTGTGTAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT
GAGTTAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT
CAATTAACAAAAGATTAATTAAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

17/5/251
YOL126C_homolog 337aa (SEQ ID NO 588)
MVKVAILGAAGIGQPLSLITKLNPNVDELALFVDVNVPGVADLSHINSSTQSYLPKDKEDKTLA
AALGSDULVIIIPAGVPRKGRDDELFINASIVQSLAEISIPRAFLVIVISNPVASTVIVAEFLQ
AKGYVDPRLREVTTLIDIVRANTFISQLFDQKRPBDFPNVWNGHSGEFLVPLVLSNKSQYDILISE
EOKRELIRVOFGEDVQAKNGAGSATLSMAVYAGYLAESILAAUNGKIDIVECTFIPLNDSIKGASE
ARKLVKDLDFSLPVLGNGNITLEVYDILNQISDDEKLLLEVALIEDLQXNIKEKVSFAKK

YBL072C_homolog 621bp public: 1..621 (SEQ ID NO 589)
AATGGTATTTTACAGATTCACGTCAACAAAGATCCGCCACTGTGTGCAAAAAGCCCAATTCAGAAAG
AAGGAAAGTTGAATTTAGGTAGACAAACAGCAACCAAGATTTGGTCAAAAAGAAATTCATCTGTCT
AAGAGAAAGTTGAATTTAGGTAGACAAACAGCAACCAAGATTTGGTCAAAAAGAAATTCATCTGTCT
AGAACAGAGGTGTGAACAAAATTTAGCTTTGAGTGTGAATGAACCGGTAACTTCTTGTGGGGTTC
GAAGGT
ACCAACACTTGT
CACTACGCTGT
GCCAAGATTCAGAAAGAAAGT
GTTGATCTGT
TGT

YBL072C_homolog 206aa (SEQ ID NO 590)
MGISDSRHRKSATGAKRQFRKRRFELGRPANTYIGPKRHSVTRRGNGQKRALFVETGNFWSGS
EGVSKRTIAGVYVHPNSNMLVTRNTLTGSAVVOIDATPPQWEMHNGATLGGKKGAAAHAAEVAAD
AKRSKRVKRLAARSAALIESAVDSQFSGSRLYAIVISRBQSGRCGYILIEGELATYLRBLTAKK
YBR009C_homolog 318bp public: 1..318 (SEQ ID NO 591)
AATGTAGAGTACCGGTGTAGAGAAAGGTAAAGTTTAAAGTAAAGGTGTGTGTGTGTGTGTGTGT
ATTGTAGAGTATCACTTCAAGTATTTACAAACACAGTATTCAGAAAGATTTGGCAGAGGTGTGT
AAGAGTATCTGT
AGAAGT
TTGAAGAGACAAAGGTGAACCTGT

YBR009C_homolog 105aa (SEQ ID NO 592)
MSGTRGKGGKGLGKGAHRKRLIENIQTGTRKRLRLARBGVNRSLALYEVRVVLKQLENTI
RDAVYTEHAKRRTVTSLDVVALKRGCKTLYFRG

YBR189W_homolog 489bp public: 1..489 (SEQ ID NO 593)
ATGCGCGGTGAATACCGGTTTAAAAAACAGAGGGGATTCAGAAATTTGGGTCCTCAANTGCTTAA
ATCAGAAAGCTGT
ATGCGTTGTATGAGAAATTTAGT
TTGGCTGTGAACCCAGAAATTTTGTGAACAGAAATTTTCAACCCAGTTGTGTGTGTGTGTGTGT
ACATGTATCCCTCCAGCGAGATTTGTATATCCCAACCCAGATTTGTGTGTGTGTGTGTGTGTGT
ATCCCATCAATTTAGT
GGTGTGTAGACCCGTTAGAGTTAAGAAAGAAACCAAGTTAAAGTGTGTGAAGAAAGTGTCCGAGAA
GAATTA

YBR189W_homolog 162aa (SEQ ID NO 594)
MAGEYFRRKGGNLDWNGSKCPKIRRAREFVTTRGEEKPKRIIRKVMALIRLVREGFLSEDKKLDVY
LAWNPFLIRBRFOPVFKGLGLARSIPHARVLINQSHIIVAGQIVITIPFTVRLDSQKHIDFALNSPYG
GGRAGVTKRKYQGRGSEEGAE

YBR191W_homolog 330bp public: 1..330 (SEQ ID NO 595)
ATGCCACACAAATCTACACAGTAAGCTGTATTTGTTAAGCTTCAATCTCCGTGTGTGTGT
ATCTATTAACAAAGTGTGTGTGAACAGATATCTTGAAGAGAGTTTACTTGAAGTGAACATGTAA
CACTGCTGT
GCTAAGGTGTAAACCGTTTACTTGAAGAGACAGCTGACCAAGAGGTGTCAAGATTTATCTCCACT
GAAGGTAACTTCTCAAACTTGTGCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

YBR191W_homolog 109aa (SEQ ID NO 596)
MPKRYVHGKGIYVNVKSSVGIINIKVGNRIEKRNLRVREHKHSACRQETLNVKSNAAKKREAK
ANGETVLYKROAAFRPSRLIISTEGNIPTGLAVYETFI

YCL035C_homolog 384bp public: 1..384 (SEQ ID NO 597)
ATGATAGCAAAATGCTGTATCTTGT
GCACAACTGAGAAAGAAATGCAACACTATTAATCTTCAACAAAGTGTGTATTTATTTAAACTTAT

176/251

1701531
TGTCATTTTGTGACCAAAACCAACATCTTAAATCAANATCCACAGAATCGTAGAAGTCATCA
AATTGGAATATTCGATGACGGATTGTACTATCAGAACTCAATTGATCTCTAATCTGTCATATATATG
GTGCCCAATTAATCTCATAAACGGACACACAGTTGGAGGAAATTCAGAAATCTTCCACACCAAT
GGGAAATTTGCAAGATATTTGAATCTCTCAGAAATTTGA

YCL035C_homolog_127aa (SEQ ID NO 598)
MIDKSSILAWGNLWYQPPPTAQTEKEIEHTINSHKIVTSKYCPFCDDTKHLLNEQYPQESYEVI
NINLIDIGLTIONOLYANTGOYMPPIIFNGOHVGGNSEVOOLHTNGKLOELNPKQY

YDL004w_homolog 486bp public: 1..486 (SEQ ID NO 599)
ATGTTTCAGACAAAGTTTTCGGTCAGTTCACCAATTAATTCCTTCGACACACCAAACTTATACACACG
GAGCCGCGGTGTTCAGATGCTTTGAAATATATCTTCGACACACCAAACTTATACACACG
TCCGAAGTCCAAACAGTAAACTTGCCTATCTGCAACGGTGATTTGGGTATTTTGGCCCAACCATTTCCA
TTCTGCGAACAAATTTGAGACACAGGATTTTGGAAATCATTTCCAAACAAACGGAGATCTGACCAATAC
GTCAACGCGCGGTATTCGCCATCTGCGTCCAAACGAGAAACAAATGTGACTATTTTTCGGCCATCAAGTCTCAAG
ACCGACAAATTTGATCTCTCTCGCGGTCAAAAACCTTGATTTTCGGCATGCCCAAAAGAGACAGCTGAATCTAGT
GATGAAAAGGTGCTGCTGGAAGCCAACTACGAAATTGGAAGTGTTAGTCTTTTCAACAATTTTACTAAG
TAA

YDL004w_homolog_161aa (SEQ ID NO 600)
MFRQVFRQVTKQSGVTKVTKVTEAAVSTDAKLSLALPHOTLYNDSEVQQVNLPSVNGDLGILANHP
IVEGRPELLLEIIISNGSDQVTFVSGGIAMQPGNKLTISAEAFYDQIDLSAVKNLIADAQKRAESS
DEKVAAREANIEIENLSDALDHFTK

YDR099w_homolog 795bp public: 1..795(SBQ ID NO 601)
ATGCCAGCCTCCGTTGAAGATTCCGTTTACCTTTGATATGCCCAACAGCAGAACGTTTATGAAGAA
ATGTTTGAACCAATGAAGAGCCGTTGCTCTCTGGCCAGAGATTGTTCTGTTGAAGAACGTTAATTTTATTA
TCTCTCTTACAAGATGTACTATGGTCTGCTGCTGCTCTTGGAGAAATTGTTTCACTCAATTTGAACAA
AAGAAGAAGCCAAAGGAAAATCAGAGACCAAGTTGCTTGCATCAGAGATTACCGTCGCAAGATTGAAGCT
GAATTGCTTAAAAATTTTGAAGATATTCTCTGTTGTTGAGGACCATTAATTAATCTATGCCCCAAACT
GTCAATTCAAAAGATTTTACTTACAAGATTGAAGGTTTACCAAGATATCTTGGCTGAATTTCTGTTACT
GCTCAAAAACGTGAAGAACCTCTGATTTTATCATTTAAGAGCTTTATAAGCTGCTCTTCGACGTTGCTGCTG
ACCGATTGGCCACCAACCCATCCATTTAGATTGGTTTATGATTAAGCTTCTCTGTTTCTTACTATGAA
ATTTTGAACCTCCCAAGAGAGCTTGTCTAATTAGCTTAAACAGCTTTTCAGATGCTGTTGTTGTTGATT
GAAACCTTATCTGAGATTCTACAGAGGTTCAACTTTGATTATGCAATTTATTTGAGAGATTAACCTTGACT
TTATGACCCAGATTATCTTGAAGCCCCAGCTGCCACTGAAGAGCAACAAACAATCCAGTCAAGCTCCAGCT
TGTTCACCTACCAAGAGATTAAGGCTGCTCAAGAATAAG

YDR099w_homolog 264aa (SEQ ID NO 602)
MPASREDSVYLKLAEQAEERYEEMVENKAVASSGQELSVERNLSVAYKNVIGARRASWIRVTSSTEQ
KEEKAGNEOSVALIDYRAKIAEELSKICEDTSLVSDHLITSAQSGESKVFYKKMGDHYRYLAEPAT
AKRKEAADLSLEYAKSAADVAVETPTPHPTLGLANFSTFYELLINSFDRACHLAKQAFDDDAVDL
FTT.SEDSKYSTLTLMQLRDNLTLATWDLSEAPATSEEOOSSOAPAAQPTEGRADQE

YDR399w_homolog 642bp public: 1..642(Seq ID NO 603)
ATGCTGAAATCGAGAAATATGACATTTTCGTACAAATATATACACACAGTTATGTCAAGAAATAGCCCGCT
AAGATCAAAAGAAATTAAGCGTCAGTCATGCTATTCCTATTTGGTCGGCGGTGTTTTTATTCACAGTCAAGATG
TTGGTTCCTCTTTGAAAGAACACAGGTCAACACGGTTAGAAATATAGGCTATCATATTTGCTTTTATAC
GAAGAGATTGAGAGTGAACACGGTATGAAAGCCAGGTACCCAGTTCGTCGGTACTCAATGGATTGAT
TATCATCAATCTAAATATCTGTTGTGTAATAATATGATAGTGTGATGATACCAAGA
ACCATTTTGCATATACCGACTGAGTAATTTGAAAAATGTTATGTAAGAGCCAAAGGTGCA
GATCTAAAGATACCAGTTTGGTATTTTGTGTGTCAGCAAGCAAAAGCAAGAAAGCAGAAATTG
CCAGATGATATATGGAAGACTGGTAAATATTTTCGCTGCTGTTCTGTCACAGATAGCTGGAATTGCAATAC
CCATGGGAGTCTACTGACATGTTTATCATCAATGAAGACTGAAGAACAGGAAACGATGTGTTCTCTT
CTTTCATCCACTTATGAGTAA

YDR399w_homolog_213aa (SEQ ID NO 604)
MSESEKYIYVNNIHLQCEIAPKIKFEKFDLLIATGGGFIAPMLRSLFKBPQPNVRIMAILISLY
EEISENGIEKPGTQWRQWIDYHQSGLDLVGKNVLIIDEVDTRTLTHAYASELKKDVEEQSKAKGA
DPKTKTGFIVLHDQKQKKAELPDDIMKTGNTFYAARSVPDSMIAYPWESDIIYVHQWKAEEQGNDFVL
PSSTTE

177/251

YDR18W_homolog_498bp_public: 1.498 (SEQ ID NO 605)
 ATGCTCCAAATTTGATCTCAAAATCAAGTATTCCTTTACTTACCAAGCTCTTGGTGGTGAAGTTGGT
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234/251

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235/251

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YUL166W_homolog 95aa Pathoseq: 1..95 (SEQ ID NO 730)

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YLR038C_homolog 83aa Pathoseq: 1..83 (SEQ ID NO 732)

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Human homologies

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237/251

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Figure 3 - 1

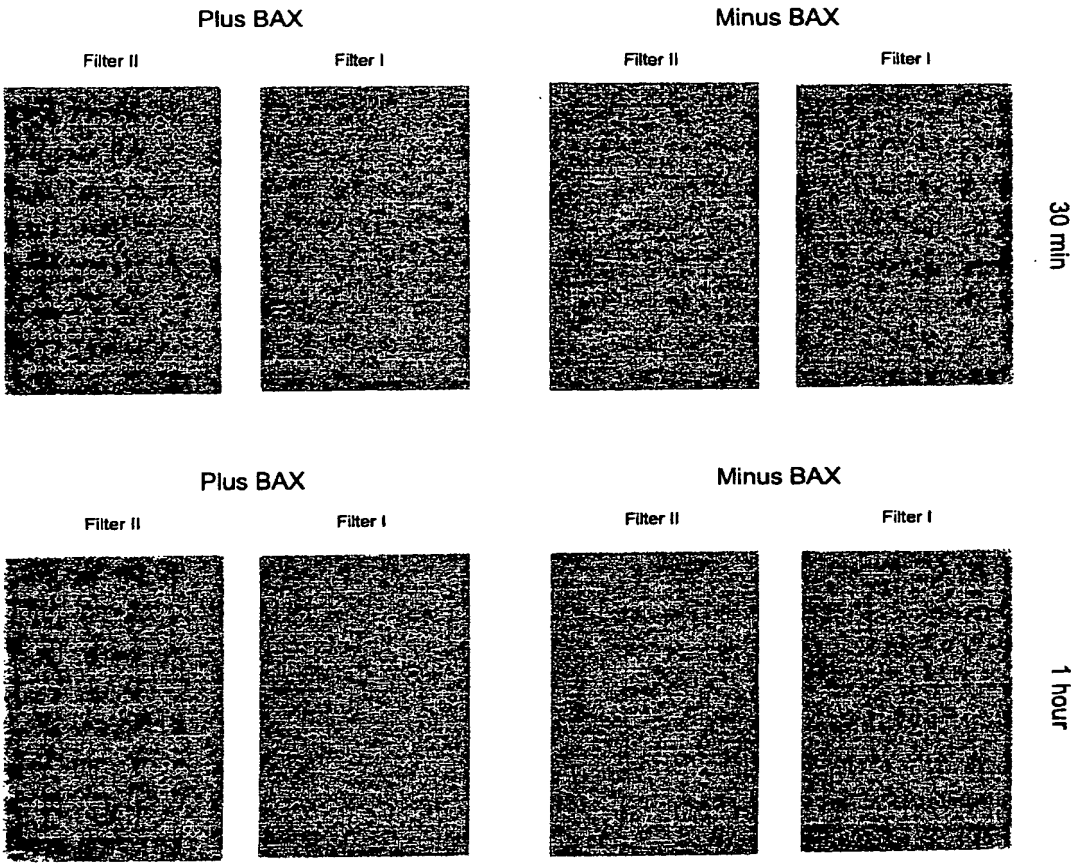
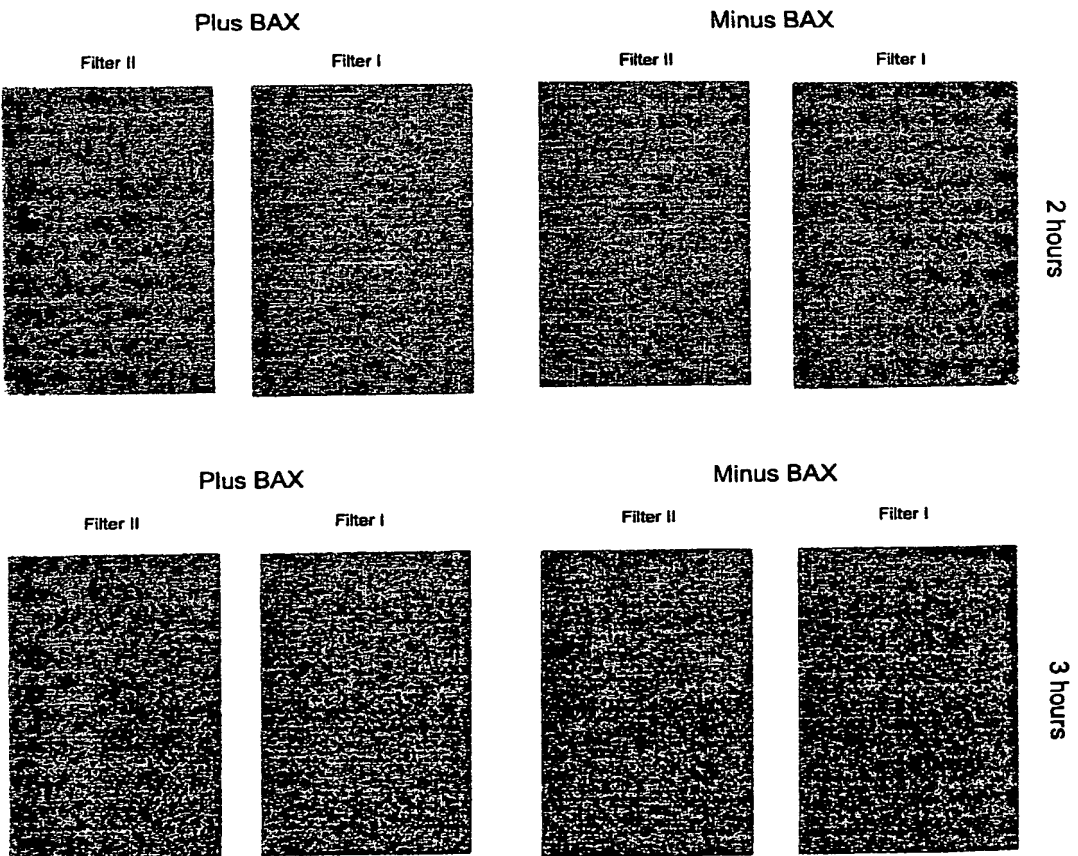
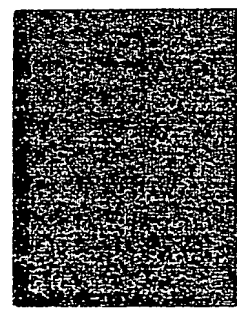


Figure 3 - 2

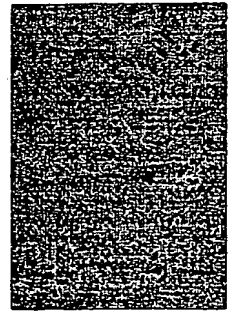


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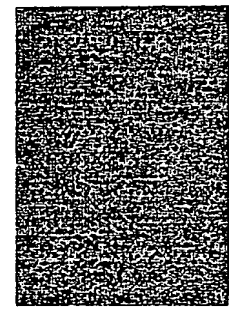


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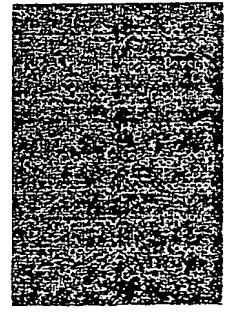


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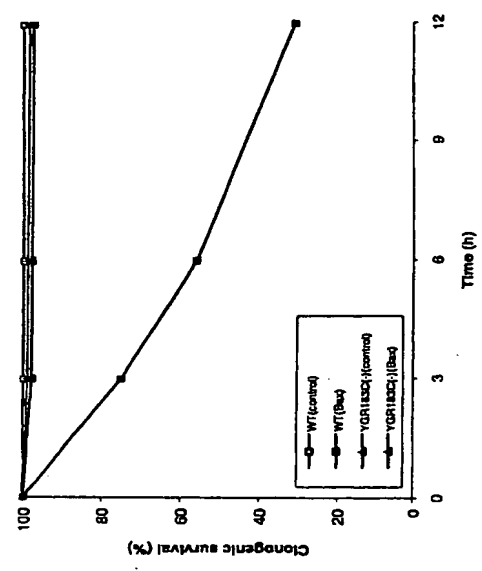
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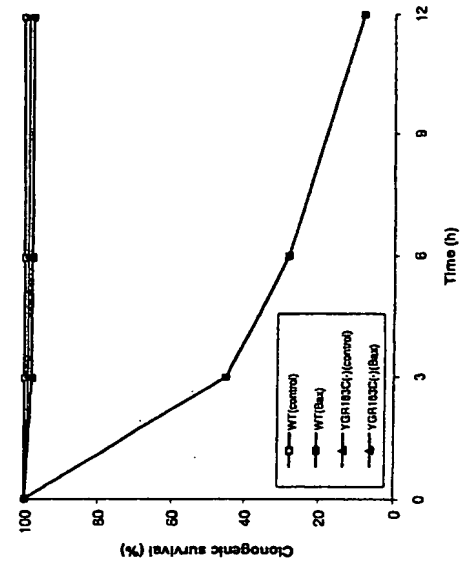


Filter II

Figure 3 - 3



(A)



(B)

Figure 4

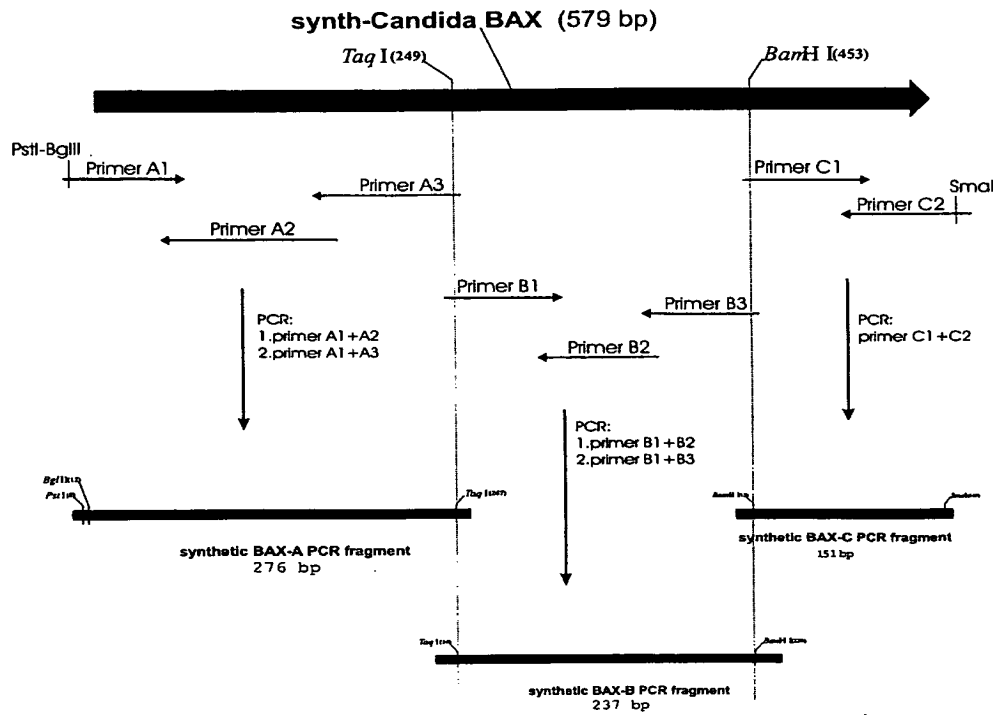


Fig. 5

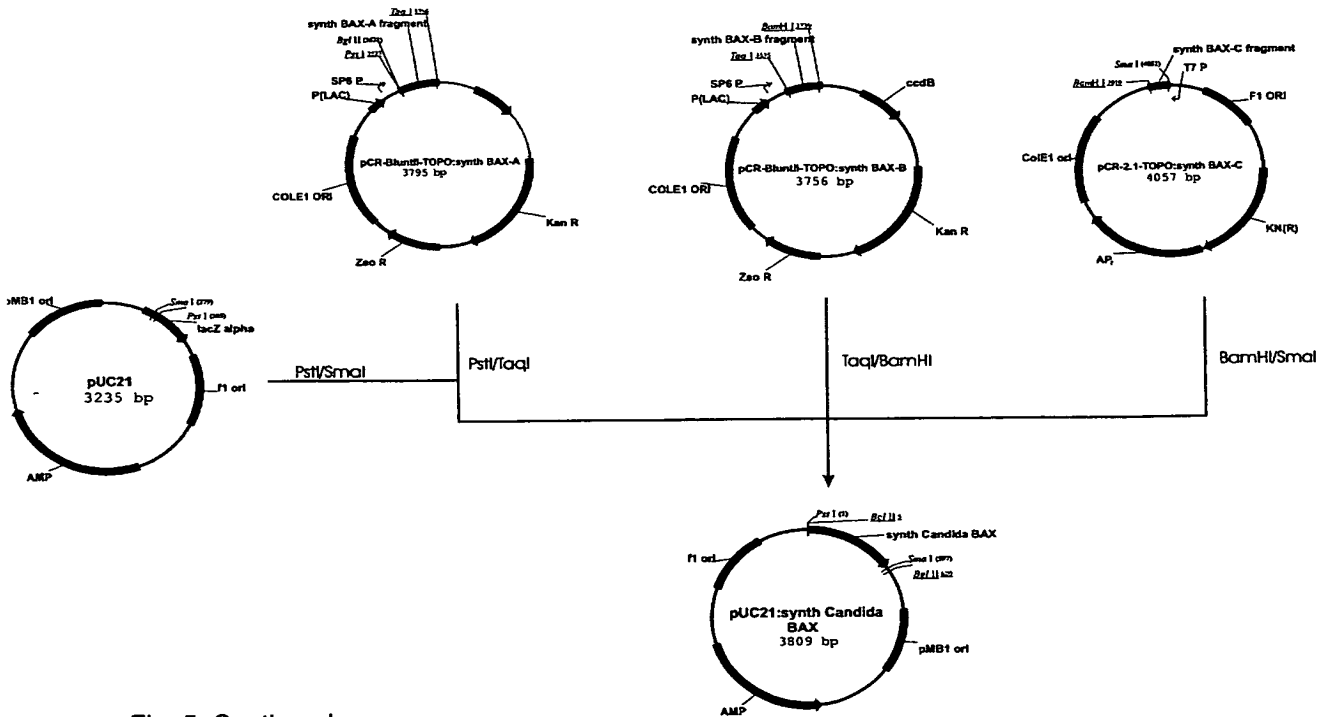


Fig. 5. Continued

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A

B

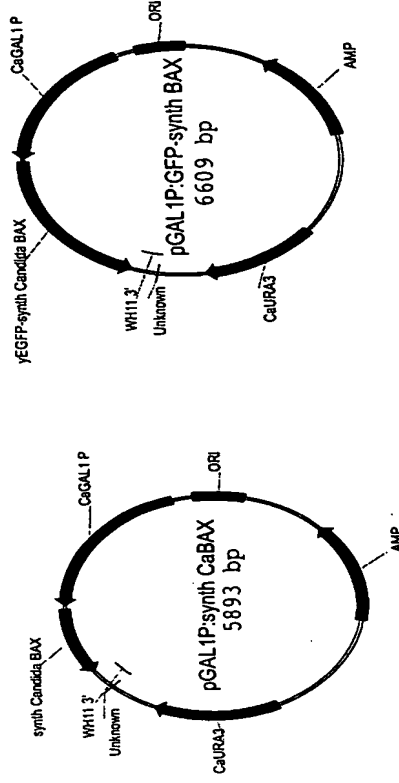


Fig. 7.

Fig. 6

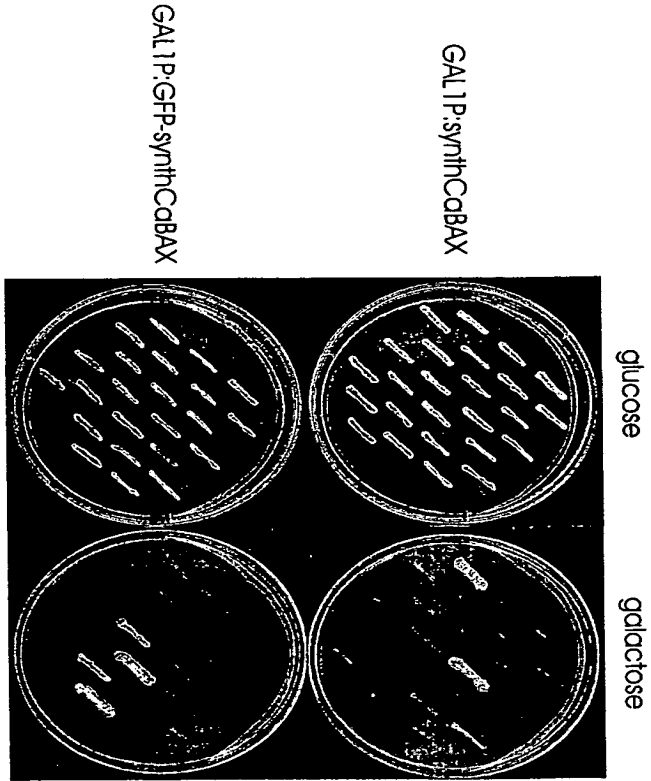


Fig. 8.

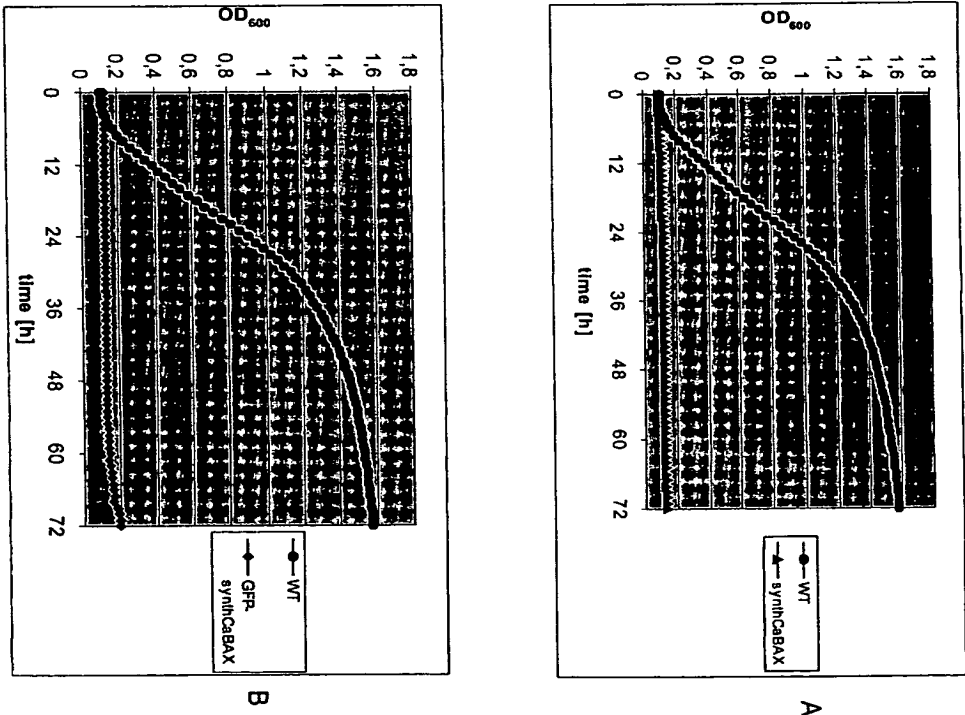


Fig. 9.

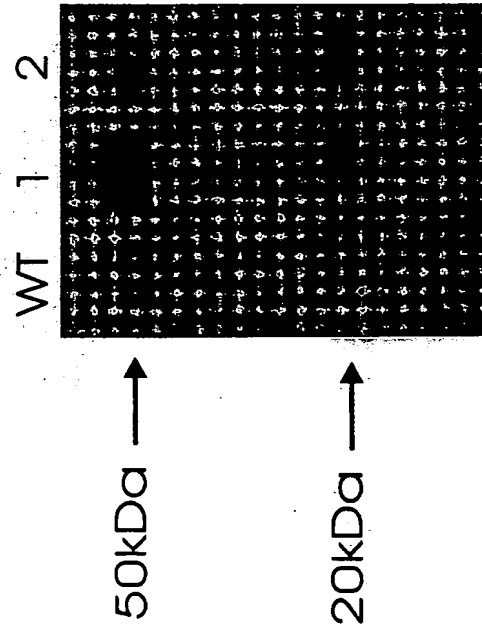


Fig. 10.

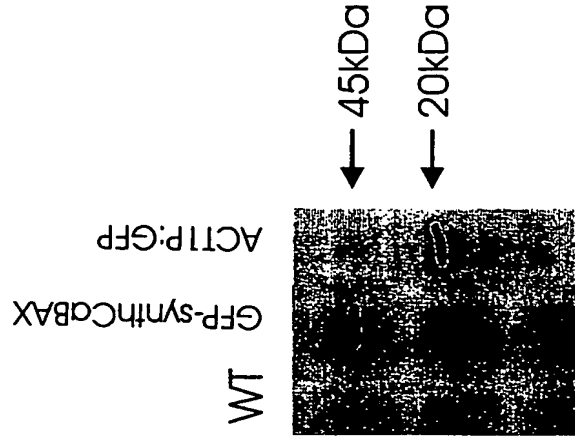


Fig. 11.

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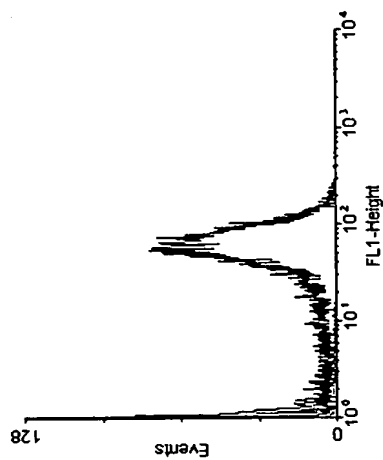
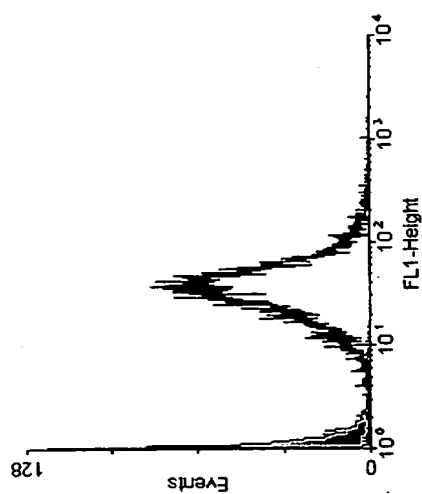


Fig.12.

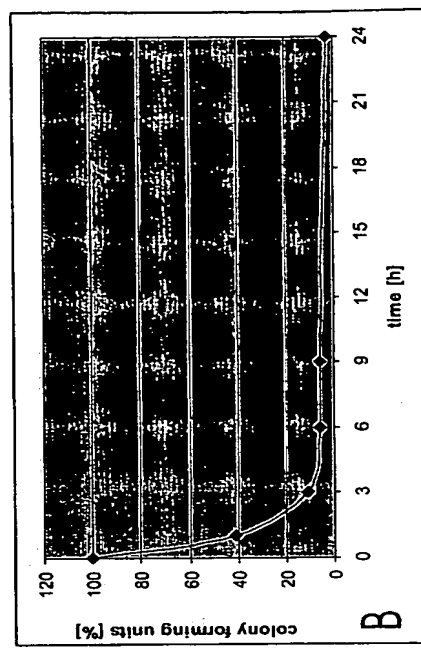
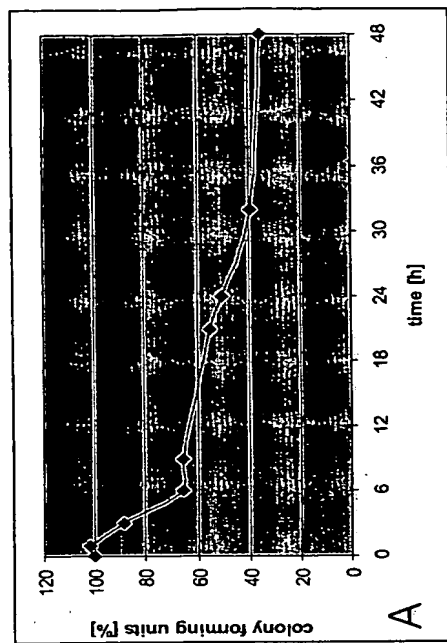


Fig. 13.

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